

	Query Match	100.0%;	Score 926;	DB 6;	Length 926;	
	Best Local Similarity	100.0%;	Pred. No. 2.1e-237;			
	Matches 926;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	CCCCCGCGTCTCTCTCCCTGTAAACATGTCATAGTGCCTGCGACACACGCGCGGGGC	60			
Db	1	CCCCCGCGTCTCTCTCTCTGTAAACATGTCATAGTGCCTGCGACACACGCGCGGGGC	60			
QY	61	GCTAGGGTTTGGCCTTCAGCCACCATGGGGGAATGGGATGAACAAGATCTTCCCGGCGCTGT	120			
Db	61	GCTAGGGTTTGGCCTTCAGCCACCATGGGGGAATGGGATGAACAAGATCTTCCCGGCGCTGT	120			
QY	121	ACATCGGCAACTTCAAAGATGCCAGAGACGCGGAAACAAATTGAGCAAGAAACAAGTGCACAC	180			
Db	121	ACATCGGCAACTTCAAAGNTGCAGAGACGCGGACAACTTGGACAGAACAGTGCACAC	180			
QY	181	ATATTCTGTCTGTCCACGATAGTGCAGGCCCTATGTTGGAGGGAGTTAAATACCTGTGCA	240			
Db	181	ATATTCTGTCTGTCCACAGATAGTGCAGGCCCTATGTTGGAGGGAGTTAAATACCTGTGCA	240			

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Db TCATTACAGAGTGCAGGCTCCGCGTGAGAGCTGCTGTACACTGCTGCGCGGGTCT 360  
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481 GACAGCTCCAGAGTTTCAGAGCATGAGTCCATCAGTATCGGCAGTGGCTGAAGGAAG 540  
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Db ACTGCTTTGGGTGGCTTGGCGCTC 926

RESULT 2  
AX068328  
LOCUS AF424702  
DEFINITION Homo sapiens JNK-stimulating phosphatase 1 (JSP1) mRNA, complete  
ACCESSION AF424702  
VERSION AX068328.1  
KEYWORDS GI:12578509  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Luche,R.M. and Wei,B.  
TITLE Dsp-3 dual-specificity phosphatase  
JOURNAL Patent: WO 0102582-A 1 11-JAN-2001;  
Ceptyr, Inc. (US)  
FEATURES  
Location/Qualifiers  
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Query Match 100.0%; Score 926; DB 6; Length 926;  
Best Local Similarity 100.0%; Pred. No. 2.le-237;  
Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCCCAGCGCTCCTCCTCCCTGTAACTGATGCGCTGCGACACACACGCGCGGGC 60  
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Db 241 TCCAGCAGCGGATTCACCATCTCAAAACCTGACACATTTTCAAAAGAAATTTAAAT 300  
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901 ACTGCTTTGGGTGGCTTGGCGCTC 926  
Db 901 ACTGCTTTGGGTGGCTTGGCGCTC 926

RESULT 3  
AF424702  
LOCUS AF424702  
DEFINITION Homo sapiens JNK-stimulating phosphatase 1 (JSP1) mRNA, complete



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 QY 557 TCATTACAGAGTCCGCGCTCCGCGTGAGAGTCTGTTGACACTGCTGCGCGGGTCT 616  
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RESULT 5  
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 ACCESSION BC022847  
 VERSION BC022847.2 GI:33872098  
 KEYWORDS MGC.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
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 REFERENCE 1 (bases 1 to 1511)  
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
 Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heieh, F.,  
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
 Sapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,  
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 Duckett, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,  
 Schenker, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
 Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
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 2 (bases 1 to 1511)  
 Strausberg, R.  
 Direct Submission  
 Submitted (04-FEB-2002) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 On Aug 19, 2003 this sequence version replaced gi:18605516.  
 Contact: MGC help desk  
 Email: [cgabs@mail.nih.gov](mailto:cgabs@mail.nih.gov)  
 Tissue Procurement: DCTD/DTP  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Institute for Systems Biology  
<http://www.systemsbio.org>  
 contact: [amadana@systemsbio.org](mailto:amadana@systemsbio.org)  
 Anup Madan, Jessica Fahey, Erin Helton, Mark Kettman, Anuradha  
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting  
 Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
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 ORIGIN  
 Query Match 99.7%; Score 922.8; DB 9; Length 1511;  
 Best Local Similarity 99.8%; Pred. No. 1.6e-236;



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QY	181	ATATTCTGTCTGTCACAGATGCGCGCTGATGTCGAGGAGTAAATACCTGTGCA	240			
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QY	241	TCCAGCAGCGGATTCACCATCTCAAACTGACAAAGACATTTCAAAGAAAGTATTAAT	300			
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RESULT 6  
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 LOCUS AX925579 1520 bp DNA linear PAT 19-DEC-2003  
 DEFINITION Sequence 1 from Patent WO03083102.  
 ACCESSION AX925579  
 VERSION AX925579.1 GI:40243937

		Query Match	Score 922.8;	DB 6;	Length 1520;
		Best Local Similarity	99.8%;	Pred. No. 1.6e-236;	
		Matches 924;	Conservative 0;	Mismatches 2;	Indels 0; Gaps 0;
QY	1	CCCCCGCGCTCCTCCTGTAACATGCGCTGCGCTGCGACACACGCGCGGGC	60		
Db	366	CCCCCGCGCTCCTCCTGTAACATGCGCTGCGCTGCGACACACGCGCGGGC	425		
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Db	486	ACATCGGCAACTTCAAAGATGCGAGAGCGGGAACAAATTCAGCAAGAACAAAGGTGACAC	545		
QY	181	ATATTCTGTCTGTCACAGATGTCGCGCTATGTTGGAGGGAGTTAAATACCTGTGCA	240		
Db	546	ATATTCTGTCTGTCACAGATGTCGCGCTATGTTGGAGGGAGTTAAATACCTGTGCA	605		
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Db	606	TCCAGCAGCGGATTCACCATCTCAAACTGACAAAGACATTTCAAAGAAAGTATTAAT	665		
QY	301	TCATTACAGAGTCCCGCTCGCGGTGAGAGTGCCTGTGTACACTGCTGCGCGGGTCT	360		
Db	666	TCATTACAGAGTCCCGCTCGCGGTGAGAGTGCCTGTGTACACTGCTGCGCGGGTCT	725		
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Db	726	CCAGGAGGTGACACTGCTGATGCGATACATCATGACCGTCACTGACTTTGGCTGGGAGG	785		
QY	421	ATGCCCTGCACACCGTGGTGGTGGAGATCTGTGCCAACCCCAACCTGCGCTTCCAGA	480		
Db	786	ATGCCCTGCACACCGTGGTGGTGGAGATCTGTGCCAACCCCAACCTGCGCTTCCAGA	845		
QY	481	GACAGCTCCAGAGTTTGAAGAGCATGAGGTGTCATAGTATCGGCAGTGGCTGAAGGAAG	540		
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QY	601	GAAATCTGAAGTTCGCGCTTCTCAGAGAGTGTAAATGACTGAAGTTTCTGAATA	660		
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KEYWORDS Homo sapiens (human).  
 SOURCE Homo sapiens  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Delaney, A.D.  
 TITLE Cancer associated protein phosphatases and their uses  
 JOURNAL Patent: WO 03083102-A 1 09-OCT-2003;  
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Db 1266 ACTGCTTGTGGGTGGCTTGGCGCTC 1291

RESULT 7
LOCUS AY249859 1532 bp mRNA linear PRI 01-APR-2004
DEFINITION Homo sapiens LMW-DSP2 mRNA, complete cds.
ACCESSION AY249859
VERSION AY249859.1 GI:37955137
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1532)
AUTHORS Mao, Y., Xie, Y. and Cheng, H.
TITLE Cloning and characterization of human LMW-DSP2 gene
JOURNAL Unpublished
AUTHORS Mao, Y., Xie, Y. and Cheng, H.
DIRECT SUBMISSION
SUBMITTED (05-MAR-2003) Institute of Genetics, Fudan University,
Handan Rd 220#, Shanghai 200433, P.R.China
FEATURES
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RESULT 8
LOCUS BD251829 1290 bp DNA linear PAT 17-JUL-2003
DEFINITION Phosphorylation effectors.
ACCESSION BD251829
VERSION BD251829.1 GI:33061599
KEYWORDS JP 2002526035-A/27.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1290)
AUTHORS Hillman, J.L., Lal, P., Tang, T.Y., Corley, N.C., Guegler, K.J.,
Baughn, M.R., Patterson, C., Bandman, O., Young, J.A., Gorgone, G.A.,
Yue, H., Azinzai, Y., Reddy, R., Lu, D.A.M. and Shih, L.L.
TITLE Phosphorylation effectors
JOURNAL Patent: JP 2002526035-A 27 20-AUG-2002;
INCYTE PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PS JP 2002526035-A/27
PD 20-AUG-2002
PF 28-JUL-1999 JP 2000562510
PR 28-JUL-1998 US 60/155213, 14-SEP-1998 US 60/155196 PR
14-OCT-1998 US 60/155239, 03-NOV-1998 US 60/106889 PR
19-NOV-1998 US 60/109093, 22-DEC-1998 US 60/113796 PR
12-JAN-1999 US 60/155233
PI JENNIFER L HILLMAN, PREETI LAL, TOM Y TANG, NEIL C CORLEY, KARL J
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DEFINITION Sequence 28369 from Patent WO0160860.
ACCESSION  CQ496502
VERSION    CQ496502.1 GI:41462121
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE  1
            Schlegel,R., Endege,W.O. and Monahan,J.E.
            Genes differentially expressed in human prostate cancer and their
            use
JOURNAL    Patent: WO 0160860-A 28369 23-AUG-2001;
            Millennium Predictive Medicine, Inc. (US)
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DEFINITION Homo sapiens mitogen-activated protein kinase phosphatase x (MKPX)
            mRNA, complete cds.
ACCESSION  AF165519
VERSION    AF165519.1 GI:9294744
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SOURCE     Homo sapiens
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REFERENCE  1
            (bases 1 to 1092)
            Gu,J., Huang,Q., Yu,Y., Xu,S., Wang,Y., Han,Z., Chen,Z., Zhou,J.,
            Tu,Y., Gu,W., Fu,G. and Huang,C.
            Novel genes expressed in hematopoietic stem/progenitor cells from
            Myelodysplastic Syndromes patient
TITLE

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JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1092)  
 AUTHORS Gu, J., Huang, Q., Yu, Y., Xu, S., Wang, Y., Han, Z. and Chen, Z.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-JUL-1999) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P.R. China  
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 IMAGE:3905407), complete cds.  
 ACCESSION BC016844  
 VERSION BC016844.1 GI:16877148  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE  
 1 (bases 1 to 851)  
 AUTHORS  
 Strausberg, R.D., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
 Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K.,  
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F.,  
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
 Shapeton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,  
 Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J.,  
 Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,  
 McKernan, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
 Vialalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
 Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,  
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shetchenko, Y.,  
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
 Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smalish, D.E.,  
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
 Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 22388257  
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 2 (bases 1 to 851)  
 Strausberg, R.  
 Direct Submission  
 Submitted (05-NOV-2001) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: The I.M.A.G.E. Consortium (ILNL)  
 Center, Stanford University School of Medicine, Stanford, CA 94305  
 Web site: <http://www-shgc.stanford.edu>  
 Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,

R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
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DEFINITION Sequence 5 from Patent WO0112819.  
ACCESSION AX086008  
VERSION AX086008.1 GI:13275835  
KEYWORDS  
SOURCE Mus sp.  
ORGANISM Mus sp.  
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Lioubin, M.  
Plowman, G.D., Martinez, R., Whyte, D., Hill, R., Flanagan, P. and  
Protein phosphatases and diagnosis and treatment of  
phosphatase-related disorders  
JOURNAL Patent: WO 0112819-A 5 22-FEB-2001;  
Sugen, Inc. (US)  
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Query Match 60.8%; Score 563.2; DB 6; Length 1067;  
Best Local Similarity 84.1%; Pred. No. 6.2e-140;  
Matches 690; Conservative 0; Mismatches 108; Indels 22; Gaps 4;  
Qy 51 CGGCGGCGGCTAGCGTTCGCCCTTCAGCCACCATGGGGAATGGATGAACAAGATCCTG 110  
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Qy 171 AAGGTGACACATATTCTGTCTGCCAGATAGTGCAGGCTATTTGGAGGGAGTTAAA 230  
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Qy 231 TACTGTGCAATCCAGCAGCGGATTCCATCTCAAACTCAAGACATTTCAAAGAA 290  
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Qy 291 AGTATTAATTCATTCAGAGTCCGGCTCCGGGTGAGAGCTGCCTTGTACACTGCTG 350  
Db 249 AGCATTAATTTCAATTCATGATGTCGATCCGATCCAGGGTGGAGCTGTCTTTGACATTTG 308  
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RESULT 14
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LOCUS Mus musculus dual specificity phosphatase TS-DSP2 mRNA, complete
DEFINITION
ACCESSION AF237619
VERSION AF237619.1 GI:13183068
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS Aoyama,K., Nagata,M., Oshima,K., Matsuda,T. and Aoki,N.
TITLE Molecular cloning and characterization of a novel dual specificity
JOURNAL phosphatase, LMW-DSP2, that lacks the cdc25 homology domain
MEDLINE J. Biol. Chem. 276 (29), 27575-27583 (2001)
PUBMED 21347909
11346645
REFERENCE 2 (bases 1 to 1067)
AUTHORS Aoyama,K., Matsuda,T. and Aoki,N.
TITLE Direct Submission
JOURNAL Submitted (19-FEB-2000) Applied Molecular Biosciences, Nagoya
University, Furo-cho, Chikusa-ku, Nagoya, Aichi 464-8601, Japan
FEATURES
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Query Match 60.5%; Score 560.2; DB 10; Length 1067;
Best Local Similarity 85.5%; Pred. No. 4e-139;
Matches 678; Conservative 0; Mismatches 93; Indels 22; Gaps 4;

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Db 82 GACGCAAGAGATGCAGAACAGTTGAGCAGGAAACAAGGTGACACACATTTCTTCTGTGCAC 141
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QY 618 GCCTTTCTCAGAGACTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 677
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QY 732 GATTTGTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 783
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RESULT 15
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LOCUS Sequence 25 from Patent WO0102582.
DEFINITION
ACCESSION AX068352
VERSION AX068352.1 GI:12578520
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Luche,R.M. and Wei,B.
TITLE Dsp-3 dual-specificity phosphatase
JOURNAL Patent: WO 0102582-A 25 11-JAN-2001;
Ceptyr, Inc. (US)
FEATURES
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ORIGIN

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Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Title: US-10-658-661-1

Perfect score: 926

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

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Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_NA.\*

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- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	70	7.6	743	4	US-09-270-767-12522
3	62.6	6.8	1830	4	US-09-557-921-1
4	59.8	6.5	1746	4	US-09-949-016-5068
5	59.8	6.5	2473	4	US-09-949-016-623
6	58.4	6.3	2000	4	US-09-016-434-1291
7	58.4	6.3	2000	4	US-09-919-497-10
8	58.4	6.3	2015	4	US-09-949-016-4969
9	57.8	6.2	1619	4	US-09-702-705-801
10	57.8	6.2	1619	4	US-09-736-457-801
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24	57	6.2	1212	4	US-09-976-594-663
25	56.2	6.1	1238	2	US-08-530-290-11
26	56.2	6.1	1238	4	US-09-702-705-803
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32	56.2	6.1	1987	2	US-08-990-379-1	Sequence 1, Appli
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34	56.2	6.1	2064	4	US-09-702-705-825	Sequence 825, App
35	56.2	6.1	2064	4	US-09-736-457-825	Sequence 825, App
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43	56.2	6.1	2109	4	US-09-671-325-826	Sequence 826, App
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ALIGNMENTS

RESULT 1  
US-09-513-999C-16851/c  
; Sequence 16851, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duciart, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: 59 US2 REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 16851  
; LENGTH: 315  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-513-999C-16851

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Db	102	ATGGGGGAATGGGATGAACAAGATCCTGCCCTTCCCT	68			

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; Sequence 12522, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 12522  
; LENGTH: 743

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; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-12522

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Matches 212; Conservative 0; Mismatches 205; Indels 9; Gaps 15;

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Qy 157 AATTGACCAAGAAACAAGGTGACACATATTTCTGTCTGTCCACGATAGTCCAGGCGCTA 216
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97 CGTTGAAAAAGTACAATAATAAAGATGTTTGAATGTGACACCAAGATTTGCCAAATAAGT 155
Qy 217 T-----GGAGGGAGTTAAATACCTGTGCTCATCCACAGCAGCGGATTCACCATCTCAA 267
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157 TCAAGGAGTCGGCGGACATCAAGTATCTGCAGATTCGATCACGGATCACTACTACAAA 216
Qy 268 ACCTGACAGACATTTCAAAGAAAGTATTAATTCATTCACAGATGCGCGGTCCGCGGTG 327
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217 ATTTGGCCATACATTTCCCGGATGCCATACAGATTTATAGAGAAAGCGCGTCCGCAAGCT 276
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Qy 388 ACATCATGACCGTCACTGACTTTGGCTGGGAGGATGCCCTGCACACCGTGCCTGGGA 447
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337 ACTTGATGTCACACGCGGGGCTGAGTCTCAACGACGCGCTTCGGATGCTGCGGACCGGA 396
Qy 448 GATCCTGTGCCAACCCCAAGCTGGGCTCCAGAGACAGCTCCAGAGATTTGAGAGCATG 507
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397 AGCCGGATGTATCGCCCAACTTCACATTCATGCAGCAGCTGCTGCTCTCGAGAGCCAA 456
Qy 508 AGGTCC 513
Db 457 TGCGCC 462

RESULT 3
US-09-557-921-1
; Sequence 1, Application US/09557921
; Patent No. 6551810
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wel, So
; TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.416
; CURRENT APPLICATION NUMBER: US/09/557,921
; CURRENT FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1830
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-557-921-1

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Qy	286	AAGAAACTATTAAATTCATTACACAGTCCGGCTCCGGGTGAGAGCTGCTTTGACACT	345		
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Db      1309 GCCAGGCTGGGGTCTCCGGTCCCGCCACCATCGTCATCGTTACTTGATGAAGCACACTC 1368
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QY      466 ACGTGGGCTTCCAGAGACAGCTCCAGGAGTTTGAGAA 502
Db      1429 ACCTTAACCTTCATGGGCAGTTGCTAGAGTTCGAGGA 1465

RESULT 4
US-09-949-016-5068
; Sequence 5068, Application US/09949016
; Patent NO. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5068
; LENGTH: 1746
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US-09-949-016-5068

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Db	151	ACTACAAATGGATTCCTGTGGAAGACAGCCACACGGCTGACATTAGCTCCCACTTTCAAG	210	
Qy	289	AAAGTATTAATTCATTACAGGTGCCGGTCCCGGTGAGAGTGCTGTGTACACTGCC	348	
Db	211	AAGCAATAGACTTCATTGACTGTGTGCAGGGAAAGGGAGGCAAGGTCTGTGTCCACTGTG	270	
Qy	349	TGGCCGGGGTCTCCAGGAGGGTGCACACTGGTGTATCGGATACATCATGACCGTCACTGACT	408	
Db	271	AGGCTGGGATCTCCCGTTACCCACCACTGTCATGGCTTACCTTATGAAGACCAAGCAGT	330	
Qy	409	TTGGCTGGGAGGATGCCCTGCACACCTGGTGTCTGGGAGATCTGTGCCAACCCCAAGC	468	
Db	331	TCCGCTTGAAGGAGGCCCTTCGATTACATCAAGCAGAGGAGGAGCATGTGTCGCCCCAAT	390	
Qy	469	TGGCTTTCCAGACACAGCTCCAGGAGTTGA	499	
Db	391	TTGGCTTCATGGGCCAGCTCTGTCAGTACGA	421	

```

RESULT 5
US-09-949-016-623.
; Sequence 623, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14

```

; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 623  
 ; LENGTH: 2473  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; US-09-949-016-623

Query Match 6.5%; Score 59.8; DB 4; Length 2473;  
 Best Local Similarity 51.3%; Pred. No. 1.3e-07;  
 Matches 139; Conservative 0; Mismatches 132; Indels 0; Gaps 0;  
 Qy 229 AATACCTGTGTCATCCACAGCGGATTCCACATCTCAAAACCTGACAGACATTTCAAAG 288  
 Db 881 ACTCAAAATGATCCCTGTGAAGACAGACACACGGCTGACATTAGCTCCACATTTCAAG 940  
 Qy 289 AAAGTATTAAATTCATTCACAGATGCGGCTCCGGGTGAGAGCTGCTGTACACTGCC 348  
 Db 941 AAGCAATAGACTTTCATTGACTGTGTGTCAGGAAAGAGGCAAGGTCTGTGTCACCTGTG 1000  
 Qy 349 TGGCGGGGTCTCCAGGAGGTGACACTGTGATCGCATACATCATGACCGTCACTGACT 408  
 Db 1001 AGGCTGGGATCTCCCGTTTCAACCCACATCTGATGGCTTACCTATGAAGACCAAGCAGT 1060  
 Qy 409 TTGGCTGGAGGATGCCCTGCACACCGTGCCTGTGGGAGATCTGTGCCAACCCCAACG 468  
 Db 1061 TCCGCTGAAGAGGCTCTCGATTACATCAAGACAGAGGAGGATGCTCTCGCCCACT 1120  
 Qy 469 TGGGCTTCACAGACAGCTCAGAGTTTGA 499  
 Db 1121 TTGGCTTCATGGCCAGCTCCTGCAGTACGA 1151

RESULT 6  
 US-09-016-434-1291  
 ; Sequence 1291, Application US/09016434  
 ; Patent No. 6500938  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Janice Au-Young  
 ; APPLICANT: Jeffrey J. Seilhamer  
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
 ; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
 ; NUMBER OF SEQUENCES: 1490  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
 ; STREET: 3174 PORTER DRIVE  
 ; CITY: PALO ALTO  
 ; STATE: CALIFORNIA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/016,434  
 ; FILING DATE: HEREWITH  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Zeller, Karen J.  
 ; REGISTRATION NUMBER: 37,071  
 ; REFERENCE/DOCKET NUMBER: PA-0002 US

; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (650) 855-0555  
 ; TELEFAX: (650) 845-4166  
 ; INFORMATION FOR SEQ ID NO: 1291:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2000 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: GENBANK  
 ; CLONE: 929980  
 ; US-09-016-434-1291

Query Match 6.3%; Score 58.4; DB 4; Length 2000;  
 Best Local Similarity 48.8%; Pred. No. 3.1e-07;  
 Matches 158; Conservative 0; Mismatches 166; Indels 0; Gaps 0;  
 Qy 197 CGATAGTCCAGGCTATGTTGGAGGAGTTAAATACCTGTGCATCCAGCAGCGGATTC 256  
 Db 857 CAATTGTCCCAACCATTTTGAGGGTCACTACAGTACAAGAGCATCCCTGTGGAGGACAA 916  
 Qy 257 ACCATCTCAAAACCTGCAAGACATTTCAAGAAAGTATTAAATTCATTACAGAGTCCG 316  
 Db 917 CCACAGGCGACATCAGCTCCTGGTTCAACGAGGCCATTTGACTTCATAGACTCCATCAA 976  
 Qy 317 GCTCCGGGTGAGAGTGCCTTTGTACACTGCTGCGGGGTCTCCAGGAGCGTGACACT 376  
 Db 977 GAATGCTGGAGGAGGTGTTTGTCCACTGCGAGGAGGCATTTCCCGGTGAGCCACCAT 1036  
 Qy 377 GGTGATCGCATACATCATGACCGTCACTGCTTGGCTGGGAGGATGCCCTGCACACCGT 436  
 Db 1037 CTGCTTGTCTTACCTTATGAGGACTAATCGAGTCAAGCTGAGCGGCTTTGAGTTGT 1096  
 Qy 437 GCGTCTGGGAGATCTGTGCCAACCCCAAGCTGGGCTTCCAGAGACAGCTCCAGGAGTT 496  
 Db 1097 GAAGCAGAGCGAGCATCATCTCTCCCAACTTCAGCTTTCATGGGCGAGCTGCTGCAGTT 1156  
 Qy 497 TGAGAAGCATGAGTCCCATCAGTA 520  
 Db 1157 TGAGTCCAGGTGCTGGCTCCGCA 1180

RESULT 7  
 US-09-919-497-10  
 ; Sequence 10, Application US/09919497  
 ; Patent No. 6773883  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mutter, George L.  
 ; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER  
 ; FILE REFERENCE: B0801/7225  
 ; CURRENT APPLICATION NUMBER: US/09/919,497  
 ; CURRENT FILING DATE: 2001-07-31  
 ; PRIOR APPLICATION NUMBER: US 60/221,735  
 ; PRIOR FILING DATE: 2000-07-31  
 ; NUMBER OF SEQ ID NOS: 100  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 10  
 ; LENGTH: 2000  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-919-497-10

Query Match 6.3%; Score 58.4; DB 4; Length 2000;  
 Best Local Similarity 48.8%; Pred. No. 3.1e-07;  
 Matches 158; Conservative 0; Mismatches 166; Indels 0; Gaps 0;  
 Qy 197 CGATAGTCCAGGCTATGTTGGAGGAGTTAAATACCTGTGCATCCAGCAGCGGATTC 256  
 Db 857 CAATTGTCCCAACCATTTTGAGGGTCACTACAGTACAAGAGCATCCCTGTGGAGGACAA 916  
 Qy 257 ACCATCTCAAAACCTGCAAGACATTTCAAGAAAGTATTAAATTCATTACAGAGTCCG 316

Db 917 CCACAGGCGACATCAGCTCCTGGTTCAACAGGCGCATTCAGTTCATAGACTCCATCA 976  
 Qy 317 GCTCGCGGTGAGAGCTGCCCTTGTAACCTGCTGCGCGGGGTCTCCAGGAGCGTGACACT 376  
 Db 977 GAATGCTGGAGGAAGGGTGTGTTCACCTGCGCAGGAGCATTTCCCGGTGAGCCACCAT 1036  
 Qy 377 GGTGATCGCATACATCATGACCGTCACTGACTTTGGCTGGGAGGATGCCCTGCACACCGT 436  
 Db 1037 CTGCGCTTGTACCTTATGAGGACTAATCGAGTCAAGCTGGACGAGGCTTTGAGTTTGT 1096  
 Qy 437 GCGTGTGGGAGATCCTGTGCCAACCCCAAGCTGGCTTCCAGAGACAGCTCCAGGAGTT 496  
 Db 1097 GAAGCAGAGGCGAAGCATCATCTCTCCCACTTCAGCTTCATGGCCAGCTGCTGCAGTT 1156  
 Qy 497 TGAGAAGCATGAGGTCCATCAGTA 520  
 Db 1157 TGAGTCCCAAGTGTGGCTCGCA 1180

RESULT 8  
 US-09-949-016-4969  
 ; Sequence 4969, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 4969  
 ; LENGTH: 2015  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-09-949-016-4969

Query Match 6.3%; Score 58.4; DB 4; Length 2015;  
 Best Local Similarity 48.8%; Pred. No. 3.1e-07;  
 Matches 158; Conservative 0; Mismatches 166; Indels 0; Gaps 0;  
 Qy 197 CGATAGTCCAGGCTATGTTGGAGGAGTTAAATACCTGTGCATCCAGCAGCGGATTC 256  
 Db 872 CAATGTCCCAACCACTTTGAGGGTCACTACAGTACAAGAGCATCCCTGTGGAGGACAA 931  
 Qy 257 ACCATCTCAAAACCTGACAGACATTTCAAGAAAGTATTAAATTCATTCACAGTGCCG 316  
 Db 932 CCACAGGCGACATCAGCTCCTGGTTCAAGAGGCGCATTCATTCATAGACTCCATCA 991  
 Qy 317 GCTCGCGGTGAGAGCTGCCCTTGTAACCTGCTGCGCGGGGTCTCCAGGAGCGTGACACT 376  
 Db 992 GAATGCTGGAGGAAGGGTGTGTTCACCTGCGCAGGAGCATTTCCCGGTGAGCCACCAT 1051  
 Qy 377 GGTGATCGCATACATCATGACCGTCACTGACTTTGGCTGGGAGGATGCCCTGCACACCGT 436  
 Db 1052 CTGCGCTTGTACCTTATGAGGACTAATCGAGTCAAGCTGGACGAGGCTTTGAGTTTGT 1111  
 Qy 437 GCGTGTGGGAGATCCTGTGCCAACCCCAAGCTGGGCTTCCAGAGACAGCTCCAGGAGTT 496  
 Db 1112 GAAGCAGAGGCGAAGCATCATCTCTCCCACTTCAGCTTCATGGCCAGCTGCTGCAGTT 1171  
 Qy 497 TGAGAAGCATGAGGTCCATCAGTA 520  
 Db 1172 TGAGTCCCAAGTGTGGCTCGCA 1195

RESULT 9  
 US-09-702-705-801  
 ; Sequence 801, Application US/09702705  
 ; Patent No. 6504010  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, Tongtong  
 ; APPLICANT: Bangur, Chaitanya S.  
 ; APPLICANT: Lodes, Michael A.  
 ; APPLICANT: Fanger, Gary  
 ; APPLICANT: Vedvick, Tom  
 ; APPLICANT: Carter, Darrick  
 ; APPLICANT: Retter, Marc  
 ; APPLICANT: Mannion, Jane  
 ; APPLICANT: Fan, Liqun  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 ; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER  
 ; FILE REFERENCE: 210121.478C14  
 ; CURRENT APPLICATION NUMBER: US/09/702,705  
 ; CURRENT FILING DATE: 2000-10-30  
 ; NUMBER OF SEQ ID NOS: 1833  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 801  
 ; LENGTH: 1619  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-09-702-705-801

Query Match 6.2%; Score 57.8; DB 4; Length 1619;  
 Best Local Similarity 50.2%; Pred. No. 4.2e-07;  
 Matches 143; Conservative 0; Mismatches 142; Indels 0; Gaps 0;  
 Qy 227 TAAATACCTGTGATCCAGCAGCGGATTCACCATCTCAAAACCTGACAAGACATTTCAA 286  
 Db 445 TCAGTACAGTGCATCCAGTGGGAAGATAACCAAGCGGCACATCAGCTCTGGTTTCA 504  
 Qy 287 AGAAGTATTAAATTCATTCACGAGTCCCGCTCCCGGTGAGAGTCCCTTGACACTG 346  
 Db 505 GGAAGCCATAGATACATCATGTCCTGGAAGACTGCGGTGGGCGCGTCTGCTGGTGC 564  
 Qy 347 CCTGGCGGGGTCTCCAGGAGCGTGACATGTGTGATCGCATATCATATGACCGTCACTGA 406  
 Db 565 CCAGGCGGGCATCTCGCGGTCCGCCACCATCTGCTGCGCTACCTGATGATGAAGAAACG 624  
 Qy 407 CTTTGGCTGGAGGATGCCCTTGACACCCGTGCGTGTGGGAGATCTCTGTGCCAACCCCAA 466  
 Db 625 GGTGAGGCTGGAGGAGCGCTTCGAGTTTGTAAAGCAGCGCGCAGCATTTATCTCGCCAA 684  
 Qy 467 CGTGGGCTTCCAGAGACAGCTCCAGGAGTTTGAGAAGCATGAGGT 511  
 Db 685 CTTGAGCTTTCATGGGCGAGCTGTGTCAGTTTCGAGTCCAGGTGCT 729

RESULT 10  
 US-09-736-457-801  
 ; Sequence 801, Application US/09736457  
 ; Patent No. 6509448  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, Tongtong  
 ; APPLICANT: Bangur, Chaitanya S.  
 ; APPLICANT: Lodes, Michael A.  
 ; APPLICANT: Fanger, Gary  
 ; APPLICANT: Vedvick, Tom  
 ; APPLICANT: Carter, Darrick  
 ; APPLICANT: Retter, Marc  
 ; APPLICANT: Mannion, Jane  
 ; APPLICANT: Fan, Liqun  
 ; APPLICANT: Wang, Aijun  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 ; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER  
 ; FILE REFERENCE: 210121.478C15  
 ; CURRENT APPLICATION NUMBER: US/09/736,457  
 ; CURRENT FILING DATE: 2000-12-13  
 ; NUMBER OF SEQ ID NOS: 1864



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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 801
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-736-457-801

Query Match          6.2%; Score 57.8; DB 4; Length 1619;
Best Local Similarity 50.2%; Pred. No. 4.2e-07;
Matches 143; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

Qy 227 TAAATACCTGTGCATCCAGAGCGGATTCAACATCTCAAAACCTGACAGACATTTCAA 286
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
445 TCAGTACAAGTGCATCCAGTGAAGATAAACCAAGGCCGACATCAGCTCCTGGTTTCAT 504
Qy 287 AGAAGATTAAATTCATTACAGAGTCCGGCTCGGGTGGAGAGTCCCTTGTACACTG 346
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
505 GGAAGCCATAGATGATACATCGATCGCGTGAAGACTGCGTGGGCGCGTGGTGCACTG 564
Qy 347 CCTGGCGGGGTCTCCAGAGCGTGACACTGGTGATCGCATATCATGACCGTCACTGA 406
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
565 CCAGCGGGCATCTCGCGTCCGCCACCATCTGCTGCGCTACCTGATGATGAAGAAACG 624
Qy 407 CTTTGGCTGGAGAGTCCCTGACACCGTGGTGGTGGAGATCCTGTGCAACCCCAA 466
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
625 GGTGAGGCTGGAGGAGGCTTCGAGTTCGTTAAGCAGCGCGCGCAGCATTTATCTCGCCAA 684
Qy 467 CGTGGCTTCCAGAGACAGCTCCAGGAGTTTGAGAGCATGAGCT 511
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
685 CTTGAGCTTTCATGGGGCAGCTGCTGCAAGTTCGAGTCCAGGTGCT 729

RESULT 11
US-09-614-124B-801
; Sequence 801, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614.124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 801
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-614-124B-801

Query Match          6.2%; Score 57.8; DB 4; Length 1619;
Best Local Similarity 50.2%; Pred. No. 4.2e-07;
Matches 143; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

Qy 227 TAAATACCTGTGCATCCAGAGCGGATTCAACATCTCAAAACCTGACAGACATTTCAA 286
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
445 TCAGTACAAGTGCATCCAGTGAAGATAAACCAAGGCCGACATCAGCTCCTGGTTTCAT 504
Qy 287 AGAAGATTAAATTCATTACAGAGTCCGGCTCGGGTGGAGAGTCCCTTGTACACTG 346
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
505 GGAAGCCATAGATGATACATCGATCGCGTGAAGACTGCGTGGGCGCGTGGTGCACTG 564
Qy 347 CCTGGCGGGGTCTCCAGAGCGTGACACTGGTGATCGCATATCATGACCGTCACTGA 406
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
565 CCAGCGGGCATCTCGCGTCCGCCACCATCTGCTGCGCTACCTGATGATGAAGAAACG 624
Qy 407 CTTTGGCTGGAGAGTCCCTGACACCGTGGTGGTGGAGATCCTGTGCAACCCCAA 466
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
625 GGTGAGGCTGGAGGAGGCTTCGAGTTCGTTAAGCAGCGCGCGCAGCATTTATCTCGCCAA 684
Qy 467 CGTGGCTTCCAGAGACAGCTCCAGGAGTTTGAGAGCATGAGCT 511
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
685 CTTGAGCTTTCATGGGGCAGCTGCTGCAAGTTCGAGTCCAGGTGCT 729

RESULT 12
US-09-671-325-801
; Sequence 801, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671.325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 801
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-671-325-801

Query Match          6.2%; Score 57.8; DB 4; Length 1619;
Best Local Similarity 50.2%; Pred. No. 4.2e-07;
Matches 143; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

Qy 227 TAAATACCTGTGCATCCAGAGCGGATTCAACATCTCAAAACCTGACAGACATTTCAA 286
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
445 TCAGTACAAGTGCATCCAGTGAAGATAAACCAAGGCCGACATCAGCTCCTGGTTTCAT 504
Qy 287 AGAAGATTAAATTCATTACAGAGTCCGGCTCGGGTGGAGAGTCCCTTGTACACTG 346
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
505 GGAAGCCATAGATGATACATCGATCGCGTGAAGACTGCGTGGGCGCGTGGTGCACTG 564
Qy 347 CCTGGCGGGGTCTCCAGAGCGTGACACTGGTGATCGCATATCATGACCGTCACTGA 406
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
565 CCAGCGGGCATCTCGCGTCCGCCACCATCTGCTGCGCTACCTGATGATGAAGAAACG 624
Qy 407 CTTTGGCTGGAGAGTCCCTGACACCGTGGTGGTGGAGATCCTGTGCAACCCCAA 466
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
625 GGTGAGGCTGGAGGAGGCTTCGAGTTCGTTAAGCAGCGCGCGCAGCATTTATCTCGCCAA 684
Qy 467 CGTGGCTTCCAGAGACAGCTCCAGGAGTTTGAGAGCATGAGCT 511
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
685 CTTGAGCTTTCATGGGGCAGCTGCTGCAAGTTCGAGTCCAGGTGCT 729

RESULT 13
US-09-589-184-801
; Sequence 801, Application US/09589184
; Patent No. 6686447
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick

```

```

Qy 407 CTTTGGCTGGAGAGTCCCTGACACCGTGGTGGAGATCCTGTGCAACCCCAA 466
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
625 GGTGAGGCTGGAGGAGGCTTCGAGTTCGTTAAGCAGCGCGCGCAGCATTTATCTCGCCAA 684
Qy 467 CGTGGCTTCCAGAGACAGCTCCAGGAGTTTGAGAGCATGAGCT 511
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
685 CTTGAGCTTTCATGGGGCAGCTGCTGCAAGTTCGAGTCCAGGTGCT 729

RESULT 12
US-09-671-325-801
; Sequence 801, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671.325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 801
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-671-325-801

Query Match          6.2%; Score 57.8; DB 4; Length 1619;
Best Local Similarity 50.2%; Pred. No. 4.2e-07;
Matches 143; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

Qy 227 TAAATACCTGTGCATCCAGAGCGGATTCAACATCTCAAAACCTGACAGACATTTCAA 286
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
445 TCAGTACAAGTGCATCCAGTGAAGATAAACCAAGGCCGACATCAGCTCCTGGTTTCAT 504
Qy 287 AGAAGATTAAATTCATTACAGAGTCCGGCTCGGGTGGAGAGTCCCTTGTACACTG 346
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
505 GGAAGCCATAGATGATACATCGATCGCGTGAAGACTGCGTGGGCGCGTGGTGCACTG 564
Qy 347 CCTGGCGGGGTCTCCAGAGCGTGACACTGGTGATCGCATATCATGACCGTCACTGA 406
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
565 CCAGCGGGCATCTCGCGTCCGCCACCATCTGCTGCGCTACCTGATGATGAAGAAACG 624
Qy 407 CTTTGGCTGGAGAGTCCCTGACACCGTGGTGGTGGAGATCCTGTGCAACCCCAA 466
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
625 GGTGAGGCTGGAGGAGGCTTCGAGTTCGTTAAGCAGCGCGCGCAGCATTTATCTCGCCAA 684
Qy 467 CGTGGCTTCCAGAGACAGCTCCAGGAGTTTGAGAGCATGAGCT 511
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
685 CTTGAGCTTTCATGGGGCAGCTGCTGCAAGTTCGAGTCCAGGTGCT 729

RESULT 13
US-09-589-184-801
; Sequence 801, Application US/09589184
; Patent No. 6686447
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick

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; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C8
; CURRENT APPLICATION NUMBER: US/09/589,184
; CURRENT FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 827
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 801
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-589-184-801

Query Match      6.2%; Score 57.8; DB 4; Length 1619;
Best Local Similarity 50.2%; Pred. No. 4.2e-07;
Matches 143; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

QY 227 TAAATACCTGTGCATCCAGCAGCGGATTCACCATCTCAAAACCTGACAAGACATTTCAA 286
Db 445 TCAGTACAAAGTGCATCCAGTGGGAAGATACCAAGCCGACATCAGCTCCTGGTTTCAT 504
QY 287 AGAAAGTATTAAATTCATTACAGAGTCCGCTCGCGGTGAGAGCTGCCCTTGTACACTG 346
Db 505 GGAAGCCATAGAGTACATCGATGCGTGAAGGACTGCCGTGGGCGCGTGTGCTGGTCACTG 564
QY 347 CTGGCCGGGTCTCCAGGAGCGTGACACTGGTGATCGCATACATCATGACCGTCACTGA 406
Db 565 CCAGCGGGGCATCTCGCGGTCCGACCATCTGCTGGCCCTACCTGATGATGAAGAAACG 624
QY 407 CTTTGGCTGGAGGATGCCCTGCACACCGTGGTGGGAGATCCTGTGCAACCCCAA 466
Db 625 GGTGAGGCTGGAGGAGCGCTTCGAGTTCGTTAAGCAGCGCGCAGCATTTATCTGCCCAA 684
QY 467 CGTGGGCTTCCAGACAGCTCCAGGAGTTTGAGAAGCATGAGGT 511
Db 685 CTTGAGCTTTCAGTGGGAGCTGCTGAGTTCGAGTTCAGTCCAGGTGCT 729

RESULT 15
US-09-016-434-1100
; Sequence 1100, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1255784
; US-09-016-434-1100

Query Match      6.2%; Score 57.8; DB 4; Length 2240;
Best Local Similarity 50.2%; Pred. No. 5.1e-07;
Matches 143; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

QY 227 TAAATACCTGTGCATCCAGCAGCGGATTCACCATCTCAAAACCTGACAAGACATTTCAA 286
Db 445 TCAGTACAAAGTGCATCCAGTGGGAAGATACCAAGCCGACATCAGCTCCTGGTTTCAT 504
QY 287 AGAAAGTATTAAATTCATTACAGAGTCCGCTCGCGGTGAGAGCTGCCCTTGTACACTG 346
Db 505 GGAAGCCATAGAGTACATCGATGCGTGAAGGACTGCCGTGGGCGCGTGTGCTGGTCACTG 564
QY 347 CTGGCCGGGTCTCCAGGAGCGTGACACTGGTGATCGCATACATCATGACCGTCACTGA 406
Db 565 CCAGCGGGGCATCTCGCGGTCCGACCATCTGCTGGCCCTACCTGATGATGAAGAAACG 624
QY 407 CTTTGGCTGGAGGATGCCCTGCACACCGTGGTGGGAGATCCTGTGCAACCCCAA 466
Db 625 GGTGAGGCTGGAGGAGCGCTTCGAGTTCGTTAAGCAGCGCGCAGCATTTATCTGCCCAA 684
QY 467 CGTGGGCTTCCAGACAGCTCCAGGAGTTTGAGAAGCATGAGGT 511
Db 685 CTTGAGCTTTCAGTGGGAGCTGCTGAGTTCGAGTTCAGTCCAGGTGCT 729

RESULT 14
US-09-658-824-801
; Sequence 801, Application US/09658824
; Patent No. 6746846
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C11
; CURRENT APPLICATION NUMBER: US/09/658,824
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 1788
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 801
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-658-824-801

Query Match      6.2%; Score 57.8; DB 4; Length 1619;
Best Local Similarity 50.2%; Pred. No. 4.2e-07;
Matches 143; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

QY 227 TAAATACCTGTGCATCCAGCAGCGGATTCACCATCTCAAAACCTGACAAGACATTTCAA 286
Db 445 TCAGTACAAAGTGCATCCAGTGGGAAGATACCAAGCCGACATCAGCTCCTGGTTTCAT 504
QY 287 AGAAAGTATTAAATTCATTACAGAGTCCGCTCGCGGTGAGAGCTGCCCTTGTACACTG 346
Db 505 GGAAGCCATAGAGTACATCGATGCGTGAAGGACTGCCGTGGGCGCGTGTGCTGGTCACTG 564
QY 347 CTGGCCGGGTCTCCAGGAGCGTGACACTGGTGATCGCATACATCATGACCGTCACTGA 406
Db 565 CCAGCGGGGCATCTCGCGGTCCGACCATCTGCTGGCCCTACCTGATGATGAAGAAACG 624
QY 407 CTTTGGCTGGAGGATGCCCTGCACACCGTGGTGGGAGATCCTGTGCAACCCCAA 466
Db 625 GGTGAGGCTGGAGGAGCGCTTCGAGTTCGTTAAGCAGCGCGCAGCATTTATCTGCCCAA 684
QY 467 CGTGGGCTTCCAGACAGCTCCAGGAGTTTGAGAAGCATGAGGT 511
Db 685 CTTGAGCTTTCAGTGGGAGCTGCTGAGTTCGAGTTCAGTCCAGGTGCT 729
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Db      839 TCAGTACAAGTGCATCCCGAGTGAAGATAAACCAAGGCCGACATCAGCTCCTGGTTTCAT 898
Qy      287 AGAAAGTATTAATTCATTACGAGTGC CGGCTCCGGTGAGAGCTGCCTTGTACTACTG 346
Db      899 GGAAGCCATAGAGTACATCGATCCGCTGAAGACTGCCGTGGGCGGTGCTGGTGCACTG 958
Qy      347 CCTGGCCGGGTCTCCAGGAGCGTGACACTGGTGATCGCATCATGACCGTCACTGA 406
Db      959 CCAGGCGGGCATCTCGCGGTCCGCCACCACATCTGCCCTGACCTGATGATGAAGAAACG 1018
Qy      407 CTTTGGCTGGGAGGATGCCCTGCACACCGTGGTGGTGGATCCTGTGCCAACCCCAA 466
Db      1019 GGTGAGGCTGGAGGAGGCCCTTCGAGTTCTTAAGCAGCGCCGACGATCATCTGCCCAA 1078
Qy      467 CGTGGGCTTCCAGAGACAGCTCCAGAGTTTGAGAAGCATGAGGT 511
Db      1079 CTTGAGCTTCATGGGACAGCTGCTGAGTTCCAGTTCAGTCCCGAGGTGCT 1123

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Search completed: July 21, 2005, 18:05:38  
Job time : 373 secs

**THIS PAGE BLANK (USPTO)**

Result No.	Score	Query Match	Length	DB	ID	Description
1	926	100.0	926	14	US-10-151-320-34	Sequence 34, Appl
2	936	100.0	926	18	US-10-444-795B-778	Sequence 778, App
3	924	99.8	1187	14	US-10-103-313-239	Sequence 239, App
4	923.6	99.7	1187	17	US-10-264-237-1406	Sequence 1406, Ap
5	922.8	99.7	1520	15	US-10-287-806-1	Sequence 1, Appl
6	894.2	96.6	1161	20	US-10-357-930-22534	Sequence 22534, A
7	894.2	96.6	1161	20	US-10-357-930-28369	Sequence 28369, A

	Query Match	100.0%;	Score 926;	DB 14;	Length 926;	
	Best Local Similarity	100.0%;	Pred. No. 7.2e-278;			
	Matches 926;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0	
Oy	1	CCCCGGCGCTCCTCCTCTGTAACATGCCATAGTGGCGCTGGCAACACACGGCCGGGGC	60			
Db	1	CCCCGGCGCTCCTCCTCTGTAACATGCCATAGTGGCGCTGGCAACACACGGCCGGGGC	60			
Oy	61	GCTAGCGTTGCGCTTCAGCCACCATGGGGAATGGGATGAACAGATCTGCCCGGCCCTGT	120			
Db	61	GCTAGCGTTGCGCTTCAGCCACCATGGGGAATGGGATGAACAGATCTGCCCGGCCCTGT	120			

## ALIGNMENTS

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QY 121 ACATCGGCAACTTCAAAAGATGCCAGAGACGGGACCAATTCAGCAAGCAACAGGTGCAC 180
Db 121 ACATCGGCAACTTCAAAAGATGCCAGAGACGGGACCAATTCAGCAAGCAACAGGTGCAC 180
QY 181 ATATTCTGTCTGTCCACGATAGTGCAGGCCCTATGTTGGAGGGAGTTAAATACCTGTGCA 240
Db 181 ATATTCTGTCTGTCCACGATAGTGCAGGCCCTATGTTGGAGGGAGTTAAATACCTGTGCA 240
QY 241 TCCAGAGCGGATTCACCATCTCAAAACCTGACAGACATTTCAAGAAAGATTTAAAT 300
Db 241 TCCAGAGCGGATTCACCATCTCAAAACCTGACAGACATTTCAAGAAAGATTTAAAT 300
QY 301 TCATTTCAGAGTGCAGGCTCCGCGTGAGAGTGCCTTTGTACATCTGCTGCCCGGGTCT 360
Db 301 TCATTTCAGAGTGCAGGCTCCGCGTGAGAGTGCCTTTGTACATCTGCTGCCCGGGTCT 360
QY 361 CCAGAGCGTGACACTGGTGATCGCATACATCATGACCGTCACTGACTTTGGCTGGGAGG 420
Db 361 CCAGAGCGTGACACTGGTGATCGCATACATCATGACCGTCACTGACTTTGGCTGGGAGG 420
QY 421 ATGCCCTGCACACCGTGGTGTGGAGATCCTGTGCGCAACCCCAACGTTGGCTTCAGAA 480
Db 421 ATGCCCTGCACACCGTGGTGTGGAGATCCTGTGCGCAACCCCAACGTTGGCTTCAGAA 480
QY 481 GACAGCTCCAGAGTTTCAGAGCATGAGTCCATCAGTATCGGCAGTGGCTGAAGNAG 540
Db 481 GACAGCTCCAGAGTTTCAGAGCATGAGTCCATCAGTATCGGCAGTGGCTGAAGNAG 540
QY 541 AATATGGAGAGAGCCCTTTGAGAGATGACAGAGAGGAGGAGGAGGAGGAGGAGGAGG 600
Db 541 AATATGGAGAGAGCCCTTTGAGAGATGACAGAGAGGAGGAGGAGGAGGAGGAGGAGG 600
QY 601 GAAATTCGAAATTCGAGGCTTTCTCAGAGACTGTAATGACCTGAAGTTTCTGAAATA 660
Db 601 GAAATTCGAAATTCGAGGCTTTCTCAGAGACTGTAATGACCTGAAGTTTCTGAAATA 660
QY 661 TTGCAAAACCCGAGAGTTTAGGCTGGTCTGCCAAAGAGGAGGAGGAGGAGGAGGAGG 720
Db 661 TTGCAAAACCCGAGAGTTTAGGCTGGTCTGCCAAAGAGGAGGAGGAGGAGGAGGAGG 720
QY 721 TATCAGTAGTGAATTTGTAACCTTTGTTTTCATTTGAAGCTGAATATATAGTAGTCATG 780
Db 721 TATCAGTAGTGAATTTGTAACCTTTGTTTTCATTTGAAGCTGAATATATAGTAGTCATG 780
QY 781 TTTATGTTGAGAACTAAGGATATTCTTTAGCAAGAGAAATATTTTCCCTTTATCCCCAC 840
Db 781 TTTATGTTGAGAACTAAGGATATTCTTTAGCAAGAGAAATATTTTCCCTTTATCCCCAC 840
QY 841 TGCTGTGGAGGTTTCGTGTACCTCGCTTGGATGCTGTGAAGATCCCGGGAGCCTTGCGC 900
Db 841 TGCTGTGGAGGTTTCGTGTACCTCGCTTGGATGCTGTGAAGATCCCGGGAGCCTTGCGC 900
QY 901 ACTGCTTGTGGTGGCTTGGCGCTC 926
Db 901 ACTGCTTGTGGTGGCTTGGCGCTC 926
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## RESULT 2

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US-10-444-795B-778
; Sequence 778, Application US/10444795B
; Publication No. US20040077574A1
; GENERAL INFORMATION:
; APPLICANT: Klinghoffer, Richard
; APPLICANT: Lewis, Stephen Patrick
; TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL
; TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE
; FILE REFERENCE: 200125.449
; CURRENT APPLICATION NUMBER: US/10/444,795B
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 842
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 778
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; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-444-795B-778
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Query Match 100.0%; Score 926; DB 18; Length 926;
Best Local Similarity 100.0%; Pred. No. 7.2e-278;
Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CCCCGCGCTCTCTCTCCCTGTAACTGTCATAGTGGCCTGCGACACACACGGCGGGGC 60
Db 1 CCCCGCGCTCTCTCTCCCTGTAACTGTCATAGTGGCCTGCGACACACACGGCGGGGC 60
QY 61 GCTAGCGTTCGCGCTTCAGCCACCATGGGAATGGGATGAACAGATCCTGCCCGGCTGT 120
Db 61 GCTAGCGTTCGCGCTTCAGCCACCATGGGAATGGGATGAACAGATCCTGCCCGGCTGT 120
QY 121 ACATCGGCAACTTCAAAAGATGCCAGAGACGGGACCAATTTGAGCAAGAAACAAGTGACAC 180
Db 121 ACATCGGCAACTTCAAAAGATGCCAGAGACGGGACCAATTTGAGCAAGAAACAAGTGACAC 180
QY 181 ATATTCTGTCTGTCCACGATAGTGCAGGCCCTATGTTGGAGGGAGTTAAATACCTGTGCA 240
Db 181 ATATTCTGTCTGTCCACGATAGTGCAGGCCCTATGTTGGAGGGAGTTAAATACCTGTGCA 240
QY 241 TCCAGAGCGGATTCACCATCTCAAAACCTGACAGACATTTCAAGAAAGATTTAAAT 300
Db 241 TCCAGAGCGGATTCACCATCTCAAAACCTGACAGACATTTCAAGAAAGATTTAAAT 300
QY 301 TCATTTCAGAGTGCAGGCTCCGCGTGAGAGTGCCTTTGTACATCTGCTGCCCGGGTCT 360
Db 301 TCATTTCAGAGTGCAGGCTCCGCGTGAGAGTGCCTTTGTACATCTGCTGCCCGGGTCT 360
QY 361 CCAGAGCGTGACACTGGTGATCGCATACATCATGACCGTCACTGACTTTGGCTGGGAGG 420
Db 361 CCAGAGCGTGACACTGGTGATCGCATACATCATGACCGTCACTGACTTTGGCTGGGAGG 420
QY 421 ATGCCCTGCACACCGTGGTGTGGAGATCCTGTGCGCAACCCCAACGTTGGCTTCAGAA 480
Db 421 ATGCCCTGCACACCGTGGTGTGGAGATCCTGTGCGCAACCCCAACGTTGGCTTCAGAA 480
QY 481 GACAGCTCCAGGAGTTTGAAGACATGAGGTCCATCAGTATCGGCAGTGGCTGAAGGAG 540
Db 481 GACAGCTCCAGGAGTTTGAAGACATGAGGTCCATCAGTATCGGCAGTGGCTGAAGGAG 540
QY 541 AATATGGAGAGAGCCCTTTGAGAGATGACAGAGAGGAGGAGGAGGAGGAGGAGGAGG 600
Db 541 AATATGGAGAGAGCCCTTTGAGAGATGACAGAGAGGAGGAGGAGGAGGAGGAGGAGG 600
QY 601 GAAATTCGAAATTCGAGGCTTTCTCAGAGACTGTAATGACCTGAAGTTTCTGAAATA 660
Db 601 GAAATTCGAAATTCGAGGCTTTCTCAGAGACTGTAATGACCTGAAGTTTCTGAAATA 660
QY 661 TTGCAAAACCCGAGAGTTTAGGCTGGTCTGCCAAAGAGGAGGAGGAGGAGGAGGAGG 720
Db 661 TTGCAAAACCCGAGAGTTTAGGCTGGTCTGCCAAAGAGGAGGAGGAGGAGGAGGAGG 720
QY 721 TATCCAGTAGTGAATTTGTAACCTTTGTTTTCATTTGAAGCTGAATATATAGTAGTCATG 780
Db 721 TATCCAGTAGTGAATTTGTAACCTTTGTTTTCATTTGAAGCTGAATATATAGTAGTCATG 780
QY 781 TTTATGTTGAGAACTAAGGATATTCTTTAGCAAGAGAAATATTTTCCCTTTATCCCCAC 840
Db 781 TTTATGTTGAGAACTAAGGATATTCTTTAGCAAGAGAAATATTTTCCCTTTATCCCCAC 840
QY 841 TGCTGTGGAGGTTTCGTGTACCTCGCTTGGATGCTGTGAAGATCCCGGGAGCCTTGCGC 900
Db 841 TGCTGTGGAGGTTTCGTGTACCTCGCTTGGATGCTGTGAAGATCCCGGGAGCCTTGCGC 900
QY 901 ACTGCTTGTGGTGGCTTGGCGCTC 926
Db 901 ACTGCTTGTGGTGGCTTGGCGCTC 926
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Db	436	TATCCAGTAGTGAATTTGTTAAACCTTTGTTTTCATTTTGAAGCTGGAATATATACGTAGTCATG	377
Qy	781	TTTATGTTGAGAACTAAGGATATCTTTAGCAAGAGAAAAATATTTTCCCTTTATCCCCAC	840
Db	376	TTTATGTTGAGAACTAAGGATATCTTTAGCAAGAGAAAAATATTTTCCCTTTATCCCCAC	317
Qy	841	TGCTGTGGAGGTTTCTGTACCTCGCTTGGATGCTGTGAAGATCCCGGAGCCTTGGCGC	900
Db	316	TGCTGTGGAGGTTTCTGTACCTCGCTTGGATGCTGTGAAGATCCCGGAGCCTTGGCGC	257
Qy	901	ACTGCCCTTGGGTGGCTTGGCGCTC	926
Db	256	ACTGCCCTTGGGTGGCTTGGCGCTC	231
RESULT 4			
US-10-264-237-1406			
; Sequence 1406, Application US/10264237			
; Publication No. US20040009491A1			
; GENERAL INFORMATION:			
; APPLICANT: Birse et al.			
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies			
; FILE REFERENCE: PAl31P1			
; CURRENT APPLICATION NUMBER: US/10/264,237			
; CURRENT FILING DATE: 2002-10-04			
; PRIOR APPLICATION NUMBER: PCT/US01/16450			
; PRIOR FILING DATE: 2001-05-18			
; PRIOR APPLICATION NUMBER: US 60/205,515			
; PRIOR FILING DATE: 2000-05-19			
; NUMBER OF SEQ ID NOS: 2876			
; SOFTWARE: PatentIn Ver. 3.1			
; SEQ ID NO 1406			
; LENGTH: 1187			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-264-237-1406			
Query Match 99.7%; Score 923.6; DB 17; Length 1187;			
Best Local Similarity 99.7%; Pred. No. 4.7e-277;			
Matches 923; Conservative 2; Mismatches 1; Indels 0; Gaps 0			
Qy	1	CCCCCGCGCTCTCCTCCTGTAACATGCCCATAGTGCCTTGGACCAACAGCGCCGGGCG	60
Db	32	CCCCCGCGCTCTCCTCCTGTAACATGCCCATAGTGCCTTGGACCAACAGCGCCGGGCG	91
Qy	61	GCTAGCGTTCGCTTCAGCCACCATGGGAATGGATGAAACAAGATCTCTGCCCGCGCTGT	120
Db	92	GCTAGCGTTCGCTTCAGCCACCATGGGAATGGATGAAACAAGATCTCTGCCCGCGCTGT	151
Qy	121	ACATCGGCNACTTCAAAAGATGCCAGAGACGCGGAACAATTGAGCAAGAACAAAGGTGACAC	180
Db	152	ACATCGGCNACTTCAAAAGATGCCAGAGACGCGGAACAATTGAGCAAGAACAAAGGTGACAC	211
Qy	181	ATAATTCTGTCTGTCCAGATAGTGCAGGCCCTATGTTGGAGGGAGTTAAATACCTGTGCA	240
Db	212	ATAATTCTGTCTGTCCAGATAGTGCAGGCCCTATGTTGGAGGGAGTTAAATACCTGTGCA	271
Qy	241	TCCCAGCAGCGGATTCACCATCTCAAAACCTGACAAGACATTTCAAGAAAGATATTAAAT	300
Db	272	TCCCAGCAGCGGATTCACCATCTCAAAACCTGACAAGACATTTCAAGAAAGATATTAAAT	331
Qy	301	TCATTTCAGAGTGCCTGCTCCCGGTGAGAGCTGCTTGTATACATCTGCTGGCCGGGTCT	360
Db	332	TCATTTCAGAGTGCCTGCTCCCGGTGAGAGCTGCTTGTATACATCTGCTGGCCGGGTCT	391
Qy	361	CCAGGAGCGTGACACTGGTGTATGCGATACATCATGACCCGTCACTGACTTTGGCTGGGAGG	420
Db	392	CCAGGAGCGTGACACTGGTGTATGCGATACATCATGACCCGTCACTGACTTTGGCTGGGAGG	451
Qy	421	ATGCCCTGCACACCGTGGCTGCTGGAGATCCTGTGCCAACCCCAACGTGGCTTCCAGA	480
Db	452	ATGCCCTGCACACCGTGGCTGCTGGAGATCCTGTGCCAACCCCAACGTGGCTTCCAGA	511

QY 481 GACAGCTCCAGAGTTTGAAGACATGAGTCCATCAGTATCGGAGTGGCTGAAGGAG 540  
DB 512 GACAGCTCCAGAGTTTGAAGACATGAGTCCATCAGTATCGGAGTGGCTGAAGGAG 571  
QY 541 AATATGGAGAGAGCCCTTTGAGGATGAGAGAGCCAAAGAAACATTTCTGGCCGCTCCAG 600  
DB 572 AATATGGAGAGAGCCCTTTGAGGATGAGAGAGCCAAAGAAACATTTCTGGCCGCTCCAG 631  
QY 601 GAATTTCTGAAGTTCTGGCCCTTTCTCAGAAGACTGTAATGACCTGAAGTTTCTGAATA 660  
DB 632 GAATTTCTGAAGTTCTGGCCCTTTCTCAGAAGACTGTAATGACCTGAAGTTTCTGAATA 691  
QY 661 TTGCAAAACCCAGAGTTTAGGCTGGTCTGCCAAAAGAAAGAAACATGAGTTTAAAG 720  
DB 692 TTGCAAAACCCAGAGTTTAGGCTGGTCTGCCAAAAGAAAGAAACATGAGTTTAAAG 751  
QY 721 TATCCAGTAGTATTGTTAACTTTTCTTTTGAAGCTGAAATATATACGTAGTCAATG 780  
DB 752 TATCCAGTAGTATTGTTAACTTTTCTTTTGAAGCTGAAATATATACGTAGTCAATG 811  
QY 781 TTTATGTTGAGAACTTAAGGATATTCTTTAGCAAGAGAAATATTTTCCCTTTATCCCCAC 840  
DB 812 TTTATGTTGAGAACTTAAGGATATTCTTTAGCAAGAGAAATATTTTCCCTTTATCCCCAC 871  
QY 841 TGCTGTGAGAGTTTCTGACCTCGCTTGGATGCCCTGTAAGGATCCCGGAGCCTTGGCCG 900  
DB 872 TGCTGTGAGAGTTTCTGACCTCGCTTGGATGCCCTGTAAGGATCCCGGAGCCTTGGCCG 931  
QY 901 ACTGCTTGTGGTGGCTTGGCGCTC 926  
DB 932 ACTGCTTGTGGTGGCTTGGCGCTC 957

## RESULT 5

US-10-287-806-1

; Sequence 1, Application US/10287806

; Publication No. US20030148341A1

; GENERAL INFORMATION:

; APPLICANT: SIN, Wun Chey

; APPLICANT: YANG, Jianxin

; TITLE OF INVENTION: Gene Amplification and Overexpression in Cancer

; FILE REFERENCE: 38002-0038

; CURRENT APPLICATION NUMBER: US/10/287,806

; CURRENT FILING DATE: 2002-11-05

; PRIOR FILING DATE: 2001-11-15

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1

; LENGTH: 1520

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-287-806-1

Query Match 99.7%; Score 922.8; DB 15; Length 1520;  
Best Local Similarity 99.8%; Pred. No. 9.7e-277;  
Matches 924; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCGCCGCTCTCTCTCCCTGTAACATGCCATAGTGGCCCTGCGACCAACAGCGCGGGGC 60  
DB 366 CCCCGCCGCTCTCTCTCCCTGTAACATGCCATAGTGGCCCTGCGACCAACAGCGCGGGGC 425  
QY 61 GCTAGCGTTCGCTTTCAGCCACCATGCGGAATGGGATGAACAAGATCTTCCCGGCGCTGT 120  
DB 426 GCTAGCGTTCGCTTTCAGCCACCATGCGGAATGGGATGAACAAGATCTTCCCGGCGCTGT 485  
QY 121 ACATCGGAACCTCAAGATGCCAGAGCGGGAACATTTAGCAAGAACAGGTGACAC 180  
DB 486 ACATCGGAACCTCAAGATGCCAGAGCGGGAACATTTAGCAAGAACAGGTGACAC 545  
QY 181 ATATTTCTCTGTCCACCATAGTGCAGGCCCTATGTTGGAGGGAGTTAAATACCTGTGCA 240

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Qy 808 TAGCAAGAGAAAATATTTTCCCTTATCCCCACCTGCTGTGAGAGTTTCTGTACTCGCTT 867
Db 787 TAGCAAGAGAGAAAATATTTTCCCTTATCCCCACCTGCTGTGAGAGTTTCTGTACTCGCTT 846
Qy 868 GGATGCCCTGTAAAGGATCCCGGAGCCTTGGCGCACTGCTTGTGGGTGGCTTGGCGCTC 926
Db 847 GGATGCCCTGTAAAGGATCCCGGAGCCTTGGCGCACTGCTTGTGGGTGGCTTGGCGCTC 905

RESULT 7
US-10-357-930-28369
; Sequence 28369, Application US/10357930
; Publication No. US2004025908A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIORITY APPLICATION NUMBER: 09/785,276
; PRIORITY FILING DATE: 2003-02-16
; PRIORITY APPLICATION NUMBER: 60/183,319
; PRIORITY FILING DATE: 2000-02-17
; PRIORITY APPLICATION NUMBER: 60/189,862
; PRIORITY FILING DATE: 2000-03-16
; PRIORITY APPLICATION NUMBER: 60/207,454
; PRIORITY FILING DATE: 2000-05-25
; PRIORITY APPLICATION NUMBER: 60/211,314
; PRIORITY FILING DATE: 2000-06-09
; PRIORITY APPLICATION NUMBER: 60/219,007
; PRIORITY FILING DATE: 2000-07-18
; PRIORITY APPLICATION NUMBER: 60/255,281
; PRIORITY FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28369
; LENGTH: 1161
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1153, 1154, 1155, 1156, 1157, 1158, 1159, 1160, 1161
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-28369

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Qy 328 AGAGCTGCTTGTACATGCTGCTGCGGGGTCTCCAGAGCGTGACATGCTGTATCCGAT 387  
 Db |||||  
 Qy 307 AGAGCTGCTTGTACATGCTGCTGCGGGGTCTCCAGAGCGTGACATGCTGTATCCGAT 366  
 Db |||||  
 Qy 388 ACATCATGACCGTACATGCTGCTGCGGGGTCTCCAGAGCGTGACATGCTGTATCCGAT 447  
 Db |||||  
 Qy 367 ACATCATGACCGTACATGCTGCTGCGGGGTCTCCAGAGCGTGACATGCTGTATCCGAT 426  
 Db |||||  
 Qy 448 GATCCTGTGCAACCCCAACCGTGGCTTCCAGAGACAGCTCCAGAGCGTGAGAGCGATG 507  
 Db |||||  
 Qy 427 GATCCTGTGCAACCCCAACCGTGGCTTCCAGAGACAGCTCCAGAGCGTGAGAGCGATG 486  
 Db |||||  
 Qy 508 AGTTCATCATGATGCGGAGTGGCTGAGAGAGAGATGAGAGAGAGCGCTTTCAGAGATG 567  
 Db |||||  
 Qy 487 AGTTCATCATGATGCGGAGTGGCTGAGAGAGAGATGAGAGAGAGCGCTTTCAGAGATG 546  
 Db |||||  
 Qy 568 CAGAGAGAGCGCAACCAATCTGCGCGCTCCAGAGATCTGAGAGATCTGAGAGATCTGCA 627  
 Db |||||  
 Qy 547 CAGAGAGAGCGCAACCAATCTGCGCGCTCCAGAGATCTGAGAGATCTGAGAGATCTGCA 606  
 Db |||||  
 Qy 628 GAAGACTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 687  
 Db |||||  
 Qy 607 GAAGACTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 666  
 Db |||||  
 Qy 688 GCTCCCAAAAGAAAGCAATAGAGATGATGATGATGATGATGATGATGATGATGATGAT 747  
 Db |||||  
 Qy 667 GCTCCCAAAAGAAAGCAATAGAGATGATGATGATGATGATGATGATGATGATGATGAT 726  
 Db |||||  
 Qy 748 TTTTCAATTTGAAGCTGAAT 807  
 Db |||||  
 Qy 727 TTTTCAATTTGAAGCTGAAT 786  
 Db |||||  
 Qy 808 TAGCAAGAGAAATATTTTCCCTTATCCCACTGCTGAGAGATTTCTGTACCTCGCTT 867  
 Db |||||  
 Qy 787 TAGCAAGAGAAATATTTTCCCTTATCCCACTGCTGAGAGATTTCTGTACCTCGCTT 846  
 Db |||||  
 Qy 868 GGATGCTGTAAGGATCCCGGAGCTTCCCGACATGCTGCTGCTGCTGCTGCTGCTGCTGCT 926  
 Db |||||  
 Qy 847 GGATGCTGTAAGGATCCCGGAGCTTCCCGACATGCTGCTGCTGCTGCTGCTGCTGCTGCT 905  
 Db |||||

RESULT 8  
 US-10-103-313-111  
 ; Sequence 111, Application US/10103313  
 ; Publication No. US20030082758A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 ; FILE REFERENCE: PUZ07C1  
 ; CURRENT APPLICATION NUMBER: US/10/103.313  
 ; CURRENT FILING DATE: 2002-03-12  
 ; NUMBER OF SEQ ID NOS: 653  
 ; Prior Application removed - See File Wrapper or Palm  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 111  
 ; LENGTH: 910  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-103-313-111

Query Match 94.6%; Score 875.8; DB 14; Length 910;  
 Best Local Similarity 99.8%; Pred. No. 3.4e-262;  
 Matches 877; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 CCCCGCGCTCTCTCTCCCTGTAAATGATGCGCTGCGACACACACACACACACACACACAC 60  
 Db |||||  
 Qy 32 CCCCGCGCTCTCTCTCCCTGTAAATGATGCGCTGCGACACACACACACACACACACACAC 91  
 Db |||||  
 Qy 61 GCTAGCGTTCGCTTACGCCACCATGCGGAAATGGGATGAAACAGATCTGCCCCGCTGT 120  
 Db |||||  
 Qy 92 GCTAGCGTTCGCTTACGCCACCATGCGGAAATGGGATGAAACAGATCTGCCCCGCTGT 151  
 Db |||||

Qy 121 ACATCGCAACTTCAAAGATGCCAGACCGGGAACAATTTAGCAAGAAACAAGGTGACAC 180  
 Db |||||  
 Qy 152 ACATCGCAACTTCAAAGATGCCAGACCGGGAACAATTTAGCAAGAAACAAGGTGACAC 211  
 Db |||||  
 Qy 181 ATATTCCTGCTGTCCACGATAGTCCAGGCTATGTTGGAGGAGTAAATACCTGTGCA 240  
 Db |||||  
 Qy 212 ATATTCCTGCTGTCCACGATAGTCCAGGCTATGTTGGAGGAGTAAATACCTGTGCA 271  
 Db |||||  
 Qy 241 TCCAGCAGCGGATTCACCACTCTCAAACCTGACAGACATTTCAAAGAAATTAAT 300  
 Db |||||  
 Qy 272 TCCAGCAGCGGATTCACCACTCTCAAACCTGACAGACATTTCAAAGAAATTAAT 331  
 Db |||||  
 Qy 301 TCATTACAGAGTGCCTGCTCCGGTCCAGAGCTGCTTGTACACTGCTGCGCGGGTCT 360  
 Db |||||  
 Qy 332 TCATTACAGAGTGCCTGCTCCGGTCCAGAGCTGCTTGTACACTGCTGCGCGGGTCT 391  
 Db |||||  
 Qy 361 CCAGGAGCTGACATGCTGCTATCGCATACATCATGACCGTCACTGCTTGGCTGGGAGG 420  
 Db |||||  
 Qy 392 CCAGGAGCTGACATGCTGCTATCGCATACATCATGACCGTCACTGCTTGGCTGGGAGG 451  
 Db |||||  
 Qy 421 ATGCTTCGACACCGTGCCTGCTGGGAGATCTGTCGCAACCCCAACCGTGGGCTTCCAGA 480  
 Db |||||  
 Qy 452 ATGCTTCGACACCGTGCCTGCTGGGAGATCTGTCGCAACCCCAACCGTGGGCTTCCAGA 511  
 Db |||||  
 Qy 481 GACAGCTCCAGGAGTTCAGAGCATGAGCTCCATCAGTATCGGACGTGCTGAGGAGAG 540  
 Db |||||  
 Qy 512 GACAGCTCCAGGAGTTCAGAGCATGAGCTCCATCAGTATCGGACGTGCTGAGGAGAG 571  
 Db |||||  
 Qy 541 AATATGAGAGAGAGCGCTTTTCAGGATGCAGAGAGCGCAAAACATTTCTGCGCGCTCCAG 600  
 Db |||||  
 Qy 572 AATATGAGAGAGAGCGCTTTTCAGGATGCAGAGAGCGCAAAACATTTCTGCGCGCTCCAG 631  
 Db |||||  
 Qy 601 GAATTCCTGAAAGTCTGCGGCTTTCTCAGAGACTGTAATGACCTGAAGTTTCTGAAATA 660  
 Db |||||  
 Qy 632 GAATTCCTGAAAGTCTGCGGCTTTCTCAGAGACTGTAATGACCTGAAGTTTCTGAAATA 691  
 Db |||||  
 Qy 661 TTGCAAAACCCAGAGTTCAGGCTGCTGCGCAAAAGCAACACATAGAGTTTAAG 720  
 Db |||||  
 Qy 692 TTGCAAAACCCAGAGTTCAGGCTGCTGCGCAAAAGCAACACATAGAGTTTAAG 751  
 Db |||||  
 Qy 721 TATCCAGTGTGATTTGTAACCTTTGTTTTCATTGAAAGCTGAAATATATACGTAGTCATG 780  
 Db |||||  
 Qy 752 TATCCAGTGTGATTTGTAACCTTTGTTTTCATTGAAAGCTGAAATATATACGTAGTCATG 811  
 Db |||||  
 Qy 781 TTTATGTTGAGAACTAAGATATTTCTTTAGCAGAGAAATATTTTCCCTTATCCACAC 840  
 Db |||||  
 Qy 812 TTTATGTTGAGAACTAAGATATTTCTTTAGCAGAGAAATATTTTCCCTTATCCACAC 871  
 Db |||||  
 Qy 841 TGCTGTGGAGGTTTCTGTACCTGCTTGGATGCTGTAA 879  
 Db |||||  
 Qy 872 TGCTGTGGAGGTTTCTGTACCTGCTTGGATGCTGTAA 910  
 Db |||||

RESULT 9  
 US-10-803-738-1  
 ; Sequence 1, Application US/10803738  
 ; Publication No. US20050014222A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Belmont, John  
 ; APPLICANT: Fletcher, Frederick  
 ; APPLICANT: Chen, Alice  
 ; APPLICANT: Jurecic, Roland  
 ; APPLICANT: Colicos, Suzanne  
 ; APPLICANT: Tan, Tse-Hua  
 ; APPLICANT: Zhou, Guisheng  
 ; TITLE OF INVENTION: Phosphatases Which Activate Map Kinase Pathways  
 ; FILE REFERENCE: 99-383-B  
 ; CURRENT APPLICATION NUMBER: US/10/803.738  
 ; CURRENT FILING DATE: 2004-03-18  
 ; PRIOR APPLICATION NUMBER: US/09/665,819A  
 ; PRIOR FILING DATE: 2000-09-20  
 ; PRIOR APPLICATION NUMBER: US 60/155,068  
 ; PRIOR FILING DATE: 1999-09-21

NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn version 3.0

SEQ ID NO 1  
LENGTH: 1218

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (181)..(795)

US-10-803-738-1

Query Match 63.7%; Score 589.4; DB 21; Length 1218;

Best Local Similarity 99.8%; Pred. No. 1.1e-172;

Matches 590; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCCGCGCTCTCTCCCTGTAAATGATGCGCTGCGACCAACACGCGCGGCG 60  
DB 98 CCCCGCGCTCTCTCCCTGTAAATGATGCGCTGCGACCAACACGCGCGGCG 157  
QY 61 GCTAGCGTTCGCTTTCAGCCACCATGGGGAATGGGATGAACAAGATCTGCGCGCGCTGT 120  
DB 158 GCTAGCGTTCGCTTTCAGCCACCATGGGGAATGGGATGAACAAGATCTGCGCGCGCTGT 217  
QY 121 ACATCGGCAACTTCAAGATGCGAGAGCGGGAACAATTGAGCAAGAAAGGTGACAC 180  
DB 218 ACATCGGCAACTTCAAGATGCGAGAGCGGGAACAATTGAGCAAGAAAGGTGACAC 277  
QY 181 ATATTCTGTCTGTCACATAGTCCAGCGCTATGTTGGGGAGTTAAATACCTGTGCA 240  
DB 278 ATATTCTGTCTGTCACATAGTCCAGCGCTATGTTGGGGAGTTAAATACCTGTGCA 337  
QY 241 TCCAGAGCGGATTCACCATCTCAAAACCTGACAAGACATTTCAAAGAAAGTATTAAT 300  
DB 338 TCCAGAGCGGATTCACCATCTCAAAACCTGACAAGACATTTCAAAGAAAGTATTAAT 397  
QY 301 TCATTACAGTGGCGGCTCGCGGTGAGAGTGCCTTTGTACATGCTGCGCGGCTCT 360  
DB 398 TCATTACAGTGGCGGCTCGCGGTGAGAGTGCCTTTGTACATGCTGCGCGGCTCT 457  
QY 361 CCAGAGCGTGACACTGGTGATCCATCATCATGACCGTCACTGACTTTGGCTGGGAGG 420  
DB 458 CCAGAGCGTGACACTGGTGATCCATCATCATGACCGTCACTGACTTTGGCTGGGAGG 517  
QY 421 ATGCCCTGCACACCGTGGTGGGATGCTGCGCAACCCCAACCGTGGGCTTCCAGA 480  
DB 518 ATGCCCTGCACACCGTGGTGGGATGCTGCGCAACCCCAACCGTGGGCTTCCAGA 577  
QY 481 GACAGCTCCAGAGTTTGAGAAAGCATGAGTCCATCATGATCGGCGAGTGAAGGAAG 540  
DB 578 GACAGCTCCAGAGTTTGAGAAAGCATGAGTCCATCATGATCGGCGAGTGAAGGAAG 637  
QY 541 AATATGGAGAGCCCTTTGAGAGTGCAGAGAGCCAAACCAATCTGG 591  
DB 638 AATATGGAGAGCCCTTTGAGAGTGCAGAGAGCCAAACCAATCTGG 688

RESULT 10

US-10-287-806-3

Sequence 3, Application US/10287806

Publication No. US20030148341A1

GENERAL INFORMATION:

APPLICANT: SIN, Wun Chey

APPLICANT: YANG, Jianxin

TITLE OF INVENTION: Gene Amplification and Overexpression in Cancer

FILE REFERENCE: 38002-0038

CURRENT APPLICATION NUMBER: US/10/287,806

CURRENT FILING DATE: 2002-11-05

PRIOR APPLICATION NUMBER: US 60/331,394

PRIOR FILING DATE: 2001-11-15

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PatentIn version 3.2

SEQ ID NO 3

LENGTH: 555

TYPE: DNA

ORGANISM: Homo sapiens

US-10-287-806-3

Query Match 59.8%; Score 553.4; DB 15; Length 555;

Best Local Similarity 99.8%; Pred. No. 1.2e-161;

Matches 554; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 84 ATGGGGAATGGGATGAACAAGATCTGCGCGCTGTACATCGGCAACTTCAAGATGCC 143  
DB 1 ATGGGGAATGGGATGAACAAGATCTGCGCGCTGTACATCGGCAACTTCAAGATGCC 60  
QY 144 AGACACCGGAACAATTGAGCAAGAAAGGTGACATATTTCTGTCTGACGATAGT 203  
DB 61 AGACACCGGAACAATTGAGCAAGAAAGGTGACATATTTCTGTCTGACGATAGT 120  
QY 204 GCCAGGCTATGTTGGAGGAGTTAAATACCTGTGATCCAGCAGCGGATTCACCATCT 263  
DB 121 GCCAGGCTATGTTGGAGGAGTTAAATACCTGTGATCCAGCAGCGGATTCACCATCT 180  
QY 264 CAAACCTGCAAGACATTTCAAAGAAAGTATTAATAATTTCAATTCAGAGTCCGCTCCGC 323  
DB 181 CAAACCTGCAAGACATTTCAAAGAAAGTATTAATAATTTCAATTCAGAGTCCGCTCCGC 240  
QY 324 GGTGAGAGTGCCTTTGTACATGCTGCGCGGCTCTCCAGGAGCGTGACACTGGTGATC 383  
DB 241 GGTGAGAGTGCCTTTGTACATGCTGCGCGGCTCTCCAGGAGCGTGACACTGGTGATC 300  
QY 384 GCATACATCATGACCGTCACTGATTTGGCTGGGAGATGCCCTGCAACCGTGGTCT 443  
DB 301 GCATACATCATGACCGTCACTGATTTGGCTGGGAGATGCCCTGCAACCGTGGTCT 360  
QY 444 GGGAGATCTGTCGCAACCCCAACCGTGGCTTCCAGAGACAGTCCAGGAGTTTGAGAAG 503  
DB 361 GGGAGATCTGTCGCAACCCCAACCGTGGCTTCCAGAGACAGTCCAGGAGTTTGAGAAG 420  
QY 504 CATGAGTCCATCATGATCGGCTGCAAGGAAGATATGGAGAGAGCCCTTTGAG 563  
DB 421 CATGAGTCCATCATGATCGGCTGCAAGGAAGATATGGAGAGAGCCCTTTGAG 480  
QY 564 GATCAGAGAGAGCCAAACCAATTTCTGCGCTCCAGGAAATTCAGAGTTCTGGGCTTTT 623  
DB 481 GATCAGAGAGAGCCAAACCAATTTCTGCGCTCCAGGAAATTCAGAGTTCTGGGCTTTT 540  
QY 624 CTCAGAGACTGTAA 638  
DB 541 CTCAGAGACTGTAA 555

RESULT 11

US-10-104-047-1501

Sequence 1501, Application US/10104047

Publication No. US20030236392A1

GENERAL INFORMATION:

APPLICANT: HELIX RESEARCH INSTITUTE

TITLE OF INVENTION: No. US20030236392A1el full length cDNA

FILE REFERENCE: HI-A0105

CURRENT APPLICATION NUMBER: US/10/104,047

CURRENT FILING DATE: 2002-03-25

PRIOR APPLICATION NUMBER:

PRIOR FILING DATE:

NUMBER OF SEQ ID NOS: 4096

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1501

LENGTH: 2835

TYPE: DNA

ORGANISM: Homo sapiens

US-10-104-047-1501

Query Match

Best Local Similarity 100.0%; Pred. No. 8.3e-141;

Matches 488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	104	GATCCTGGCCGGCTCTGTA	CATCGGCACTTCAAGATGCCAGAGACGGCGGAACAATTTGAG	163	
Db	513	GATCCTGGCCGGCTCTGTA	CATCGGCACTTCAAGATGCCAGAGACGGCGGAACAATTTGAG	572	
Qy	164	CAAGAAACAAGGTGACACATA	TTCTGTCTGTCCACCATAGTGCAGGCGCTATGTTGGAGGG	223	
Db	573	CAAGAAACAAGGTGACACATA	TTCTGTCTGTCCACCATAGTGCAGGCGCTATGTTGGAGGG	632	
Qy	224	AGTTAAATACCTGTGTCAT	CCAGACGCGGATTCACCATCTCAAAACCTTGA	CAAGACATTT	283
Db	633	AGTTAAATACCTGTGTCAT	CCAGACGCGGATTCACCATCTCAAAACCTTGA	CAAGACATTT	692
Qy	284	CAAGAAAGTATTAAATTCATT	CACAGTGC	CGGCTCCGCGGTGAGAGCTGCTTTGTACA	343
Db	693	CAAGAAAGTATTAAATTCATT	CACAGTGC	CGGCTCCGCGGTGAGAGCTGCTTTGTACA	752
Qy	344	CTGCTGGCCGGGCTCTCCAGAGGGT	GACACTGTGTGATCGCATCATCATGACCGTGCAC	403	
Db	753	CTGCTGGCCGGGCTCTCCAGAGGGT	GACACTGTGTGATCGCATCATCATGACCGTGCAC	812	
Qy	404	TGACTTTTGGCTGGGAGGAT	GCCTCGCACCGTGGTGTCTGGGAGATCTGTGCCAACCC	463	
Db	813	TGACTTTTGGCTGGGAGGAT	GCCTCGCACCGTGGTGTCTGGGAGATCTGTGCCAACCC	872	
Qy	464	CAACGTGGGCTTCCAGAGACAGCT	CCAGAGTTTGAGAGCATGAGGTCCATCATGATCG	523	
Db	873	CAACGTGGGCTTCCAGAGACAGCT	CCAGAGTTTGAGAGCATGAGGTCCATCATGATCG	932	
Qy	524	GCAGTGGCTGAAGGAAGAA	TATGGAGAGCCCTTTG	CAGGATGCAGAGAGGCCAAAAA	583
Db	933	GCAGTGGCTGAAGGAAGAA	TATGGAGAGCCCTTTG	CAGGATGCAGAGAGGCCAAAAA	992
Qy	584	CATTCTGG	591		
Db	993	CATTCTGG	1000		

```

RESULT 12
US-803-738-3
; Sequence 3, Application US/10803738
; Publication No. US20050014222A1
; GENERAL INFORMATION:
; APPLICANT: Belmont, John
; APPLICANT: Fletcher, Frederick
; APPLICANT: Chen, Alice
; APPLICANT: Jurecic, Roland
; APPLICANT: Colicos, Suzanne
; APPLICANT: Tan, Tse-Hua
; APPLICANT: Zhou, Guisheng
; TITLE OF INVENTION: Phosphatases Which AC
; FILE REFERENCE: 99-383-B
; CURRENT APPLICATION NUMBER: US/10/803,738
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/665,819A
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US 60/155,068
; PRIOR FILING DATE: 1999-09-21
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 3010
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15)..(629)
; OTHER INFORMATION: n is a, t, c, or g
US-10-803-738-3

```

Qy	71	GCCTTGAGCCACCATGGGGAATGGAGTAAACAAGATCCTGCCCGCCTGTACATCGGCAA	130
Db	2	GCCCGGCGCGCCATGGGGAATGGGATGAGCCAGATCCTGCCCGGCCCTGTACATTTGGCAA	61
Qy	131	CTTCAAAGATGCCAGAGACGGGAAACAATTCAGCAAGAAACAAGGTGACACATATTCTGTG	190
Db	62	CTTCAAAGACGAAGAGATGCAGAACGTTGAGCAGGAACAAGGTGACACATTTCTTTC	121
Qy	191	TGTCACGATAGTGCCAGGCCCTATTGTTGGAGGGAGTTAAATACCTGTGCATCCCCAGCAGC	250
Db	122	TGTGCACGATCTGCCAGGCCCATGTTGGAGGGAGTTAAATACCTGTGTTATTCACAGCGC	181
Qy	251	GGATTCCACCATCTCAAAACCTGACAGACATTTCAAGAAAGATTAAATTCATTTCACGA	310
Db	182	AGACACACCATCTCAAAACCTGACAGACATTTCAAGAAAGATTTAAATTCATTTCATGA	241
Qy	311	GTGCGGCTCCGCGTGAGAGCTGCCCTTGATACACTGCTGCCGGGTCTCCAGAGAGGT	370
Db	242	GTGCGGACTCCAGGGTGAGAGCTGTCTTGATACATTTGCCCTGGGTCTCCAGAGAGGT	301
Qy	371	GACACTGTGTATCGCATACATCATGACCGTCACTGACTTTTGGCTGGGAGGATGCCCTGCA	430
Db	302	GACATTTGTGTATCGCATACATCATGACTGTCCAGACTTTGGCTGGGAAGATGCTTGC	361
Qy	431	CACCGTGGTCTGGGAGATCCTGTGCCAAACCCAAACCTGGGCTTCCAGAGACAGCTCCA	490
Db	362	CACTTGTTCTGGGGAGGTCCTGTGCCAAACCCAAACCTGGGCTTTCAAAGGACGCCGCA	421
Qy	491	GGAGTTTGAGAAAGATGAGTCCATCAGTATCGGAGTGGCTGAGGAAGATATGGAGA	550
Db	422	GGAGTTTGAGAAACATGAAGTGCACCAAGTATCGGCAATGGCTGAGGAAGAGTATGGAGA	481
Qy	551	GAGCCCTTTGCAGGATGCAGAAAGACCCAAACCAATTCCTGG	591
Db	482	GAACCTTTGGCGATGCAGAAAGACCAAAAATATTTCTGG	522
RESULT 13			
US-10-101-510-481			
; Sequence 481, Application US/10101510			
; Publication No. US20030148295A1			
; GENERAL INFORMATION:			
; APPLICANT: WAN, JACKSON			
; APPLICANT: WANG, YIXIN			
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE			
; FILE REFERENCE: 15117.0012			
; CURRENT APPLICATION NUMBER: US/10/101,510			
; CURRENT FILING DATE: 2002-03-20			
; PRIOR APPLICATION NUMBER: 60/276,947			
; PRIOR FILING DATE: 2001-03-20			
; NUMBER OF SEQ ID NOS: 805			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 481			
; LENGTH: 2420			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: modified base			
; LOCATION: (906)..(1002)			
; OTHER INFORMATION: a, t, c, g, other or unknown			
US-10-101-510-481			

	Query Match	40.5%	Score 375.4	DB 15	Length 2420
	Best Local Similarity	89.5%	Pred. No. 1.1e-105		
	Matches 436	Conservative	0	Mismatches 1	Indels 50
				Gaps 1	
QY	105	ATCTGCGCCGCTGTATACGCGCAACTTCAAAGATGCCAGAGACGCGGAACAATTGAGC	164		
DB	1	ATCTGCGCCGCTGTATACGCGCAACTTCAAAGATGCCAGAGACGCGGAACAATTGAGC	60		
QY	165	AAGAACAAAGGTGACACATATTTCTGTCTGTGTCACAGATAGTCCAGGCCTATGTTGGAGGA	224		
DB	61	AAGAACAAAGGTGACACATATTTCTGTCTGTGTCACAGATAGTCCAGGCCTATGTTGGAG---	117		





Qy	831	TTATCCCGCACTGCTGTGGAGGTTTCTGTACCTCGCTTGGATGCCGTAAAGGATCCCGGA	890
Db	287	TTATCCCGCACTGCTGTGGAGGTTTCTGTACCTCGCTTGGATGCCGTAAAGGATCCCGGA	346
Qy	891	GCCTTGCGCACTGCTGTGGGTTGGCTTGGCGCTC	926
Db	347	GCCTTGCGCACTGCTGTGGGTTGGCTTGGCGCTC	382

Search completed: July 21, 2005, 18:51:59  
Job time : 727 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 21, 2005, 07:55:30 ; Search time 3729 Seconds  
(without alignments)  
9452.270 Million cell updates/sec

Title: US-10-658-661-1

Perfect score: 926

Sequence: 1 cccgcgcgtctctctcct.....ttgtgggtgcttgccgcgc 926

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hic:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gsa1:\*

9: gb\_gsa2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	869.8	93.9	1066	3	CR596349 full-leng
2	853	92.1	1060	5	BX358385
3	796	86.0	895	5	BQ225790 AGENCOURT
4	763.8	82.5	879	5	BUI181268
5	755.8	81.6	953	5	BX358384
6	712.2	76.9	717	1	AV714942 AV714942
7	705	76.1	758	4	B1908832 603066403
8	681	73.5	915	2	BE868556 603444589
9	653.8	70.6	665	4	BG532390 602561902
10	644.2	69.6	694	1	AV764304 AV764304
11	622.4	67.2	655	6	CD693732 EST10255
12	607	65.6	819	6	CB995799 AGENCOURT
13	582.4	62.9	930	6	CA453928 AGENCOURT
14	569.4	61.5	751	4	BG545679 602572945
15	566	61.1	712	7	CR394735 170006001
16	560	60.5	845	5	BUI198761 DCBCQF01
17	554.4	59.9	835	5	BU603622 AGENCOURT
18	548.4	59.2	1038	5	BM922798 AGENCOURT
19	541	58.4	1088	5	BM920978 AGENCOURT
20	540.4	58.4	819	2	BE910217 601503530
21	536.4	57.9	538	6	CB215017 NISC np01
22	536.2	57.9	950	4	BG674814 602620947
23	502.2	54.2	784	7	CR792116 DKF2p469M
24	496.4	53.6	1087	5	BQ894734 AGENCOURT

C 25	494.8	53.4	715	5	BM982838	BM982838	UI-CF-EN1
C 26	493.2	53.3	715	5	BQ018732	BQ018732	UI-H-DH1-
C 27	491.2	53.0	716	6	CB852535	CB852535	UI-CF-FN0
C 28	489	52.8	504	6	CD629904	CD629904	56051849H
C 29	487.4	52.6	505	6	CD629905	CD629905	56051849H
30	479	51.7	600	4	BG800196	BG800196	2113-90 M
31	469.4	50.7	713	4	BM018391	BM018391	603646072
32	462.8	50.0	715	7	BN842339	BN842339	AGENCOURT
33	453.2	48.9	589	2	AW963729	AW963729	EST375902
34	451.4	48.7	574	5	BQ416267	BQ416267	i53a04.Y
35	450	48.6	1108	4	BM541277	BM541277	AGENCOURT
36	443.8	47.9	447	1	AA10486	AA10486	zv23b12.r
37	433.8	46.8	859	4	BI829670	BI829670	603079718
38	421.8	45.6	2252	3	BC080718	BC080718	Mus muscu
39	421.4	45.5	569	4	BI158161	BI158161	602920611
40	411.4	44.4	522	6	CB720826	CB720826	AMGNNUC:N
41	410.2	44.3	528	5	BQ416291	BQ416291	i53c10.Y
42	394.8	42.6	651	5	BUI182790	BUI182790	AGENCOURT
43	394.6	42.6	510	6	CA034663	CA034663	4000292 B
44	392.2	42.4	734	4	BG697122	BG697122	602660343
45	390.4	42.2	477	6	CA407076	CA407076	1003225 H

## ALIGNMENTS

CR596349 1066 bp mRNA linear HTC 21-JUL-2004  
full-length cDNA clone CSODI037YC10 of Placenta Cot 25-normalized  
of Homo sapiens (human).  
ACCESSION CR596349  
VERSION CR596349.1 GI:50477156  
KEYWORDS HPC; CNSLT\_cDNA.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1066)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished  
Contact: Feng Liang Email: fliang@lifetech.com URL:  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue  
Redwood City, CA 94063  
REFERENCE 2 (bases 1 to 1066)  
Genoscope.  
Direct Submission  
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr  
- Web: www.genoscope.cns.fr)  
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
into the NotI and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
FEATURES  
Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CSODI037YC10"  
/tissue="Placenta Cot 25-normalized"  
/plasmid="pCMVSPORT\_6"

Query Match 93.9%; Score 869.8; DB 3; Length 1066;  
Best Local Similarity 99.8%; Pred. No. 2.8e-243;  
Matches 871; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Oy 54 CCGGGGCGCTAGCGTTCGCTTACGCCACCACTGGGGAATGGATGAACAGATCTGCCC 113  
Db 1 CCGGGGCGCTAGCGTTCGCTTACGCCACCACTGGGGAATGGATGAACAGATCTGCCC 60

QY	114	GGCTGTACATCGGCACTTCAAGATGCCAGAGCGCGGAACAATTTGAGCAAGACAAG	173
DB	61	GGCTGTACATCGGCACTTCAAGATGCCAGAGCGCGGAACAATTTGAGCAAGACAAG	120
QY	174	GTGACACATATCTCTGTCCACCATAGTCAGCGCCTATTTGGAGGGAGTTAAATAC	233
DB	121	GTGACACATATCTCTGTCCACCATAGTCAGCGCCTATTTGGAGGGAGTTAAATAC	180
QY	234	CTGTGCATCCAGCAGCGGATTCACCATCTCAAAACCTGCAAGACATTTCAAGAAAGT	293
DB	181	CTGTGCATCCAGCAGCGGATTCACCATCTCAAAACCTGCAAGACATTTCAAGAAAGT	240
QY	294	ATTAATATTCATTCAGAGTCGGCTCCGGGTGAGACTGCTGTACATGCTGCGCC	353
DB	241	ATTAATATTCATTCAGAGTCGGCTCCGGGTGAGACTGCTGTGTACATGCTGCGCC	300
QY	354	GGGTCTCAGAGCGTGACACTGTGTATCGCATATCATGACCGTCACATGCTTTGGC	413
DB	301	GGGTCTCAGAGCGTGACACTGTGTATCGCATATCATGACCGTCACATGCTTTGGC	360
QY	414	TGGAGGATGCTTGCACACCGTGGTCTGGGATCCTGTGCCAACCCCAAGCTGGC	473
DB	361	TGGAGGATGCTTGCACACCGTGGTCTGGGATCCTGTGCCAACCCCAAGCTGGC	420
QY	474	TTCCAGACAGCTCCAGAGTTTGAAGAGCATGAGTCCATCAGTATCGGACGTGCTG	533
DB	421	TTCCAGACAGCTCCAGAGTTTGAAGAGCATGAGTCCATCAGTATCGGACGTGCTG	480
QY	534	AAGGAAGATATGGAGAGCGCTTTGAGAGATGAGAGGAGGAGGAGGAGGAGGAGG	593
DB	481	AAGGAAGATATGGAGAGCGCTTTGAGAGATGAGAGGAGGAGGAGGAGGAGGAGG	540
QY	594	GCTCAGGAATTTCTGAAGTTCTGGGCTTTCTCAGAAGACTGTAAATGACCTGAAGTTC	653
DB	541	GCTCAGGAATTTCTGAAGTTCTGGGCTTTCTCAGAAGACTGTAAATGACCTGAAGTTC	600
QY	654	TGAATATTTGMAACCCGAGGTTTGGCTGGTCTGCCAAAAGGAGGAGGAGGAGG	713
DB	601	TGAATATTTGMAACCCGAGGTTTGGCTGGTCTGCCAAAAGGAGGAGGAGGAGG	660
QY	714	GTAAAGTATCAGTATGATTTGAACTTTTTCATTTGAGCTGAATATATACGT	773
DB	661	GTAAAGTATCAGTATGATTTGAACTTTTTCATTTGAGCTGAATATATACGT	720
QY	774	AGTATGTTTATGTTGAGAACTAAGGATATTTCTTGAAGAGGAGGAGGAGGAGG	833
DB	721	AGTATGTTTATGTTGAGAACTAAGGATATTTCTTGAAGAGGAGGAGGAGGAGG	780
QY	834	TCCCACTGCTGTGGAGTTTCTGTACCTGCTGGATGCTGTAAAGGATCCCGGAGCC	893
DB	781	TCCCACTGCTGTGGAGTTTCTGTACCTGCTGGATGCTGTAAAGGATCCCGGAGCC	840
QY	894	TTGGCGCACTGCTGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	926
DB	841	TTGGCGCACTGCTGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	873
RESULT 2			
LOCUS	BX358385	1060 bp	mRNA linear EST 08-APR-2004
DEFINITION	BX358385	Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA	
ACCESSION	BX358385	clone CS01037YC10 5-PRIME, mRNA sequence.	
VERSION	BX358385.2	GI:46304699	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 1060)		
	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.		
	Full-length cDNA libraries and normalization		

JOURNAL	Unpublished (2001)		
COMMENT	On May 5, 2003 this sequence version replaced gi:30376226.		
CONTACT	Genoscope		
CONTACT	Genoscope - Centre National de Sequencage		
CONTACT	2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE		
CONTACT	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr		
CONTACT	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime		
CONTACT	end enriched, double-strand cDNA was digested with Not I and cloned		
CONTACT	into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library		
CONTACT	was normalized. Library was constructed by Life Technologies, a		
CONTACT	division of Invitrogen. This sequence belongs to sequence cluster		
CONTACT	3530.f		
CONTACT	For more information about this cluster, see		
CONTACT	http://www.genoscope.cns.fr/cdna?s=CS0D1037BB05QPl&c=3530.f.		
FEATURES	Location/Qualifiers		
source	1..1060		
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	/db_xref="taxon:9606"		
	/clone="CS0D1037YC10"		
	/tissue_type="PLACENTA COT 25-NORMALIZED"		
	/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"		
	/notes="1st strand cDNA was primed with a NotI-oligo(dT)		
	primer. Five prime end enriched, double-strand cDNA was		
	digested with Not I and cloned into the Not I and EcoR V		
	sites of the pCMVSPORT 6 vector. Library was normalized."		
ORIGIN			
Query Match	92.1%; Score 853; DB 5; Length 1060;		
Best Local Similarity	99.3%; Pred. No. 2.4e-238;		
Matches	867; Conservative 0; Mismatches 5; Indels 1; Gaps 1;		
QY	54	CCGGGGCGCTAGGCTTCGCTTCAGGCCACCATGGGGAATGGGATGAACAAGATCCTGCC	113
DB	2	CGGGATCGCTAGGCTTCGCTTCAGGCCACCATGGGGAATGGGATGAACAAGATCCTGCC	61
QY	114	GGCTGTACATTCGGCAACTTCAAGATGCCAGAGCGCGGAACAATTGAGCAAGACAAG	173
DB	62	GGCTGTACATTCGGCAACTTCAAGATGCCAGAGCGCGGAACAATTGAGCAAGACAAG	121
QY	174	GTGACACATATTCGTCTGTCCACGATAGTCAGCGCCTATGTCGAGGGAGTTAAATAC	233
DB	122	GTGACACATATTCGTCTGTCCACGATAGTCAGCGCCTATGTCGAGGGAGTTAAATAC	181
QY	234	CTGTGCATCCAGCAGCGGATTCACCATCTCAAAACCTGCAAGACATTTCAAGAAAGT	293
DB	182	CTGTGCATCCAGCAGCGGATTCACCATCTCAAAACCTGCAAGACATTTCAAGAAAGT	241
QY	294	ATTAATATTCATTCAGAGTCGGCTCCGGGTGAGACTGCTGTACACTGCTGCGCTGCC	353
DB	242	ATTAATATTCATTCAGAGTCGGCTCCGGGTGAGACTGCTGTGTACACTGCTGCGCTGCC	301
QY	354	GGGTCTCAGAGCGGTGACACTGTGTATCGCATATCATGACCGCTCACTGACTTTGGC	413
DB	302	GGGTCTCAGAGCGGTGACACTGTGTATCGCATATCATGACCGCTCACTGACTTTGGC	361
QY	414	TGGAGAGATGCTTGCACACCGTGGTCTGGGAGATCTGTGCCAACCCCAAGCTGGGC	473
DB	362	TGGAGAGATGCTTGCACACCGTGGTCTGGGAGATCTGTGCCAACCCCAAGCTGGGC	421
QY	474	TTCCAGAGACAGCTCCAGGAGTTTGAAGAGCATGAGTCCATCAGTATCGGCAGTGGCTG	533
DB	422	TTCCAGAGACAGCTCCAGGAGTTTGAAGAGCATGAGTCCATCAGTATCGGCAGTGGCTG	481
QY	534	AAGGAAGAATATGGAGAGCGCTTTTTCAGGATGCAAGAGGAGCCAAAACAATTCCTGCC	593
DB	482	AAGGAAGAATATGGAGAGCGCTTTTTCAGGATGCAAGAGGAGCCAAAACAATTCCTGCC	541
QY	594	GCTCAGGAATTCGAAGTTCGGGCTTTCTCAGAGACTGTATGTACCTGAGAGTTTC	653
DB	542	GCTCCGGGAATTCGAAGTTCGGGCTTTCTCAGAGACTGTATGTACCTGAGAGTTTC	601
QY	654	TGAATATTCGAAACCCGAGAGTTTATGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGT	712

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Db      602 TGAATATTGCAACCCACAGAGTTTAGCTGGTGCCTGCAAAAGAAAGCAACATAAG 661
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Qy      713 AGTTTAAGTATCCAGTAGTGAATTTGTAAGTGTGTTTTCATTGAGCTGATATATAG 772
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Db      662 AGTTTAAGTATCCAGTAGTGAATTTGTAAGTGTGTTTTCATTGAGCTGATATATAG 721
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Qy      773 TAGTCATGTTTATGTTGAGAACTAAGGATATTTCTTTAGCAAGAGAAATATTTTCCCTT 832
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Db      722 TAGTCATGTTTATGTTGAGAACTAAGGATATTTCTTTAGCAAGAGAAATATTTTCCCTT 781
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Qy      833 ATCCCACTGCTGTGGAGTTTCTGTAAGTGTGATGCTGTAAGATCCCGGAGC 892
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Db      782 ATCCCACTGCTGTGGAGTTTCTGTAAGTGTGATGCTGTAAGATCCCGGAGC 841
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Qy      893 CTTGCGCACTGCTTGTGGGTGGCTTGGCGCT 925
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Db      842 CTTGCGCACTGCTTGTGGGTGGCTTGGCGCT 874
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RESULT 3
B0225790
LOCUS   B0225790 7588986 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6070216
DEFINITION
ACCESSION B0225790.1 GI:20407190
VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 895)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL NIH-MGC http://mgi.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DP/Gapdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM13354 row: c column: 17
High quality sequence stop: 589.
Location/Qualifiers
1. .895
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 68"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.8 Kb. Library constructed by Life
Technologies."

ORIGIN
Query Match 86.0%; Score 796; DB 5; Length 895;
Best Local Similarity 98.7%; Pred. No. 1.2e-221;
Matches 813; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
Qy 101 CAAGATCTCGCCGGCTGTACATCGGCAACTTCAAGATGCCAGAGCGCGGAACAATT 160
Db 1 CAAGATCTCGCCGGCTGTACATCGGCAACTTCAAGATGCCAGAGCGCGGAACAATT 60
Qy 161 GAGCAAGAACAAAGGTGACACATATTTCTGTCTGCCAGTAGTGCAGGCTTATGTGA 220
Db 61 GAGCAAGAACAAAGGTGACACATATTTCTGTCTGCCAGTAGTGCAGGCTTATGTGA 120

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Qy      221 GGGAGTTAAATACCTGTGTCATCCAGCAGCGGATTCACCATCTCAAAACCTGACAAGACA 280
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Db      121 GGGAGTTAAATACCTGTGTCATCCAGCAGCGGATTCACCATCTCAAAACCTGACAAGACA 180
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Qy      281 TTTCAAGAAAAGTATTAATTCATTCACAGTGCAGGCTCCGCGGTGAGAGCTGCTGTGT 340
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Db      181 TTTCAAGAAAAGTATTAATTCATTCACAGTGCAGGCTCCGCGGTGAGAGCTGCTGTGT 240
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Qy      341 ACATGCTGCGCGGGGTCTCCAGAGCGTGCACACTGGTGATCGCATACATCATGACCGT 400
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Db      241 ACATGCTGCGCGGGGTCTCCAGAGCGTGCACACTGGTGATCGCATACATCATGACCGT 300
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Qy      401 CACTGACTTTGGCTGGGAGGATGCCCTGCACACCGTGCCTGCTGGGAGATCTGTGCGCAA 460
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Db      301 CACTGACTTTGGCTGGGAGGATGCCCTGCACACCGTGCCTGCTGGGAGATCTGTGCGCAA 360
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Qy      461 CCCCAACGTGGGCTTCCAGAGACAGCTCCAGAGTTTGAGAAGCATGAGGTCATCAGTA 520
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Qy      521 TCGCAGTGGCTGAAGGAAGATATGGAGAGAGCCCTTTGCGAGGATGCAGAAGAGCCAA 580
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Db      421 TCGCAGTGGCTGAAGGAAGATATGGAGAGAGCCCTTTGCGAGGATGCAGAAGAGCCAA 480
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Db      481 AAACATTTCTGGCGCTCCAGGAATTTCTGAAGTTCTGGGCTTTTCTCAGAAGACTGTAATG 540
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Qy      641 TACCTGAAGTTTCTGAATATTTGCAAAACCCAGAGTTTAGGCTGCTGCGCAAAAAGA 700
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Db      541 TACCTGAAGTTTCTGAATATTTGCAAAACCCAGAGTTTAGGCTGCTGCGCAAAAAGA 600
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Qy      701 AAAGCAACATAGATTTAAGTATCCAGTAGTGAATTTGTAAGTTTAACTTTTTCATTGAGGC 760
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Qy      761 TGAATATATACCTAGTCAATGTTTATGTTGAGAACTTAAGGATATTTTAGCAAGAGAAAA 820
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Db      661 TGAATATATACCTAGTCAATGTTTATGTTGAGAACTTAAGGATATTTTAGCAAGAGAAAA 720
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Qy      821 TATTTTCCCTTATCCCACTGCTGTGGAGTTTCTGTACCTGCTGCGTGGATGCTGTGAAG 880
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Db      721 TATTTTCCCTTATCCCACTGCTGTGGAGTTTCTGTACCTGCTGCGTGGATGCTGTGAAG 780
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Qy      881 GATCCC-GGGAGCCTTGGCGCACTGCTTGTGGGTGGCTTGGCG 923
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Db      781 GATCCC-GGGAGCCTTGGCGCACTGCTTGTGGGTGGCTTGGCG 824
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RESULT 4
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LOCUS   BUI81268 7938918 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6008665
DEFINITION
ACCESSION BUI81268
VERSION BUI81268.1 GI:22695252
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 879)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL NIH-MGC http://mgi.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DP/Gapdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM13354 row: c column: 17
High quality sequence stop: 589.
Location/Qualifiers
1. .895
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 68"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.8 Kb. Library constructed by Life
Technologies."

```



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QY 377 GGTGATCGCATACATCATGACCGTCACTGACTTTGGCTGGGAGGATGCCCTGCACACCGT 436
D 714 GGTGATCGCATACATCATGACCGTCACTGACTTTGGCTGGGAGGATGCCCTGCACACCGT 655
QY 437 GGTGCTGGGAGATCTGTGCGCAACCCCAACCTGCGGCTTCCAGACAGAGCTCCAGGATT 496
D 654 GGTGCTGGGAGATCTGTGCGCAACCCCAACCTGCGGCTTCCAGACAGAGCTCCAGGATT 595
QY 497 TCAGAAAGCATGAGTCCATCAGTATCGGCGAGTGGCTGAAGGAAGAAATATGGAGAGAGCC 556
D 594 TGAGAAAGCATGAGTCCATCAGTATCGGCGAGTGGCTGAAGGAAGAAATATGGAGAGAGCC 535
QY 557 TTTGAGGATGAGAGAGAGCCAAACCAATTTCTGCGCTCCAGGAATTTCTGAATTTCTG 616
D 534 TTTGAGGATGAGAGAGAGCCAAACCAATTTCTGCGCTCCAGGAATTTCTGAATTTCTG 475
QY 617 GGCCTTTCTCAGAGACTGTAATGTAACCTGAAGTTTCTGAATATATGCAACCCGACAG 676
D 474 GGCCTTTCTCAGAGACTGTAATGTAACCTGAAGTTTCTGAATATATGCAACCCGACAG 415
QY 677 TTTAGGCTGGTCTGCAAAAGAAAGCAACAT-AGAGTTTAAAGTATCCAGTAGTGATT 735
D 414 TTTAGGCTGGTCTGCAAAAGAAAGCAACAT-AGAGTTTAAAGTATCCAGTAGTGATT 355
QY 736 TGTAAACTTGTGTTTCAATTTGAAGCTGAATATATACGTAGTCACTTTATGTTGAGAACT 795
D 354 TGTAAACTTGTGTTTCAATTTGAAGCTGAATATATACGTAGTCACTTTATGTTGAGAACT 295
QY 796 AAGGATATCTTTAGAGAGAAATATATTTCCCTTATCCCACTGCTGTGGAGGTTTC 855
D 294 AAGGATATCTTTAGAGAGAAATATATTTCCCTTATCCCACTGCTGTGGAGGTTTC 235
QY 856 TGTACTCGCTGGATGCTGTAAGATCCCGGAGCCTTGCACGCTGCTGGGCTG 915
D 234 TGTACTCGCTGGATGCTGTAAGATCCCGGAGCCTTGCACGCTGCTGGGCTG 175
QY 916 GCTTGGCGCT 925
D 174 GCTTGGCGCT 165

RESULT 6
AV714942
LOCUS AV714942 DCB Homo sapiens cDNA clone DCBBJE09 5', mRNA sequence.
DEFINITION AV714942
ACCESSION AV714942.1 GI:10796459
VERSION EST.
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J.,
Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X.,
Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Lu,G., Cheng,Z. and Han,Z.
TITLE Homo sapiens cDNA DCB clones
JOURNAL Unpublished (2000)
COMMENT Contact: Zeguogang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
1..717
/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Query Match 76.9%; Score 712.2; DB 1; Length 717;
Best Local Similarity 99.6%; Pred. No. 4.1e-197;
Matches 714; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 100 ACAAGATCTCCCGGCTGTACATCGGCAATCTCAAGATGCGAGAGACCGGAACAAT 159
D 1 ACAAGATCTCCCGGCTGTACATCGGCAATCTCAAGATGCGAGAGACCGGAACAAT 60
QY 160 TGAGCAAGAACAGGTGACACATATTTCTGTCTCCAGTAGTCCAGGCTATGTTGG 219
D 61 TGAGCAAGAACAGGTGACACATATTTCTGTCTCCAGTAGTCCAGGCTATGTTGG 120
QY 220 AGGAGATTAAATACCTGTGCAATCCAGCAGCGGATTCACCATCTCAAAACCTGCAAGAC 279
D 121 AGGAGATTAAATACCTGTGCAATCCAGCAGCGGATTCACCATCTCAAAACCTGCAAGAC 180
QY 280 ATTTCAAGAAAGTATTAAATTTCAATTCAGAGTCCGCGCTCCGCGGTGAGAGCTGCCTTG 339
D 181 ATTTCAAGAAAGTATTAAATTTCAATTCAGAGTCCGCGCTCCGCGGTGAGAGCTGCCTTG 240
QY 340 TACACTGCTGGCGGGTCTCCAGGAGCGTGACACTGGTGATCGCATACATCATGACCG 399
D 241 TACACTGCTGGCGGGTCTCCAGGAGCGTGACACTGGTGATCGCATACATCATGACCG 300
QY 400 TCACCTGACTTTGGTGGGAGGATCCCTGCACACCGTGCCTGGGAGATCTTGTCGA 459
D 301 TCACCTGACTTTGGTGGGAGGATCCCTGCACACCGTGCCTGGGAGATCTTGTCGA 360
QY 460 ACCCAACGCTGGGCTTCCAGAGACAGCTCCAGGAGTTTGAAGACATGAGGTCCATCAGT 519
D 361 ACCCAACGCTGGGCTTCCAGAGACAGCTCCAGGAGTTTGAAGACATGAGGTCCATCAGT 420
QY 520 ATCGGCTGCTGAAGAGAAATATGGAGAGAGCCCTTTCCAGAGATGCGAGAGAGCCA 579
D 421 ATCGGCTGCTGAAGAGAAATATGGAGAGAGCCCTTTCCAGAGATGCGAGAGAGCCA 480
QY 580 AAAACATCTGCGCGCTCCAGGAATCTGAAGTTCTCGGCCCTTCTCAGAGAGCTGTAAT 639
D 481 AAAACATCTGCGCGCTCCAGGAATCTGAAGTTCTCGGCCCTTCTCAGAGAGCTGTAAT 540
QY 640 GTACCTGAAGTTTCTGAATAATTTGCAACCCGCGAGAGTTTAGGCTGGTGCCTCAAAAAG 699
D 541 GTACCTGAAGTTTCTGAATAATTTGCAACCCGCGAGAGTTTAGGCTGGTGCCTCAAAAAG 600
QY 700 AAAAGCAACATAGAGTTTAAGTATCCAGTAGTATTTGTAACCTGTTTTCATTTGAAG 759
D 601 AAAAGCAACATAGAGTTTAAGTATCCAGTAGTATTTGTAACCTGTTTTCATTTGAAG 660
QY 760 CTGATATATACGTAAGTATGTTTGTGAGAACTAAGGATATCTTTTACCAAGAG 816
D 661 CTGATATATACGTAAGTATGTTTGTGAGAACTAAGGATATCTTTTACCAAGAG 717

RESULT 7
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LOCUS BI908832
DEFINITION 603066403F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5215465 5',
mRNA sequence.
ACCESSION BI908832
VERSION BI908832.1 GI:16171910
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

/clone="DCBBJE09"
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/clone_lib="DCB"
/note="vector: pTriplex2; Site_1: sfIIA; Site_2: sfIIB"
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REFERENCE 1 (bases 1 to 758)  
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapsb@mail.nih.gov](mailto:cgapsb@mail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM1541 row: e column: 02  
High quality sequence stop: 736.  
Location/Qualifiers  
1..758  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5215465"  
/tissue\_type="Leukocyte"  
/lab\_host="DH10B"  
/clone\_lib="NIH MGC 118"  
/note="Vector: PCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH\_MGC Library."

ORIGIN  
Query Match 76.1%; Score 705; DB 4; Length 758;  
Best Local Similarity 98.5%; Pred. No. 5,4e-195;  
Matches 722; Conservative 0; Mismatches 10; Indels 1; Gaps 1;  
QY 195 CACGATAGTGCAGCGCTATGTTGGAGGAGTTAAATACCTGTGCATCCCGACGCGGAT 254  
Db 1 CACGATAGTGCAGCGCTATGTTGGAGGAGTTAAATACCTGTGCATCCCGACGCGGAT 60  
QY 255 TCACCATCTCAAAACCTGACAGACATTTCAAGAAAGTATTAATTCATTACAGAGTGC 314  
Db 61 TCACCATCTCAAAACCTGACAGACATTTCAAGAAAGTATTAATTCATTACAGAGTGC 120  
QY 315 CGGCTCCGGGTGAGAGTGCCTTGTACACTGCTGGCGGGGTCTCCAGGAGGTGACA 374  
Db 121 CGGCTCCGGGTGAGAGTGCCTTGTACACTGCTGGCGGGGTCTCCAGGAGGTGACA 180  
QY 375 CTGGTGATCGCATACATGACCGTCACTGACTTTGGCTGGGAGGATGCCCTGCACACC 434  
Db 181 CTGGTGATCGCATACATGACCGTCACTGACTTTGGCTGGGAGGATGCCCTGCACACC 240  
QY 435 GTGCGTGTGGAGATCTGTGCGCAACCCACGCTGGGCTTCCAGAGACAGCTCCAGGAG 494  
Db 241 GTGCGTGTGGAGATCTGTGCGCAACCCACGCTGGGCTTCCAGAGACAGCTCCAGGAG 300  
QY 495 TTTGAGAGCATGAGTCCATCAGTATCGGAGTGGCTGAAGGAAGATATGGAGAGGC 554  
Db 301 TTTGAGAGCATGAGTCCATCAGTATCGGAGTGGCTGAAGGAAGATATGGAGAGGC 360  
QY 555 CTTTTCAGGATGTCAGAGAGAGCCAAAAACATTTCTGGCGGCTTCCAGGAAATTTCTGAAGTTC 614  
Db 361 CTTTTCAGGATGTCAGAGAGAGCCAAAAACATTTCTGGCGGCTTCCAGGAAATTTCTGAAGTTC 420  
QY 615 TGGGCTTTCTCAGAAAGACTGTATGTACGTGAAGTTTCTGAA-ATATTGCAAAACCCGCA 673  
Db 421 TGGGCTTTCTCAGAAAGACTGTATGTACGTGAAGTTTCTGAAACATATTGCAAAACCCGCA 480  
QY 674 GAGTTTAGCTGGTCTGCGCAAAAGAAAGCAACATAGAGTTTAAAGTATCCAGTAGTGA 733

Db 481 GAGTTTAGCTGGTCTGCCAAAAGAAAGCAACATAGAGTTTAACTATCCAGTAGTGA 540  
QY 734 TTTGTAACACTGTTTTCATTTTGAAGCTGAATATATACGTAGTCATGTTTATGTTGAGAA 793  
Db 541 TTTGTAACACTGTTTTCATTTTGAAGCTGAATATATACGTAGTCATGTTTATGTTGAGAA 600  
QY 794 CTAAGGATATTTCTTTAGCAAGAGAGAAATATTTTCCCTTATCCCACTGCTGTGGAGGTT 853  
Db 601 CTAAGGATATTTCTTTAGCAAGAGAGAAATATTTTCCCTTATCCCACTGCTGTGGAGGTT 660  
QY 854 TCTGTACTCGCTTGGATGCTGTAAGGATCCCGGAGCCTTGGCGACACTGCTTGTGGG 913  
Db 661 ACTGTACTCGCTTGGATGCTGTAAGGATCCCGGAGCCTTGGCGACACTGCTTGTGGG 720  
QY 914 TGGCTTGGCGCTC 926  
Db 721 TGGCTTGGCGCTC 733

RESULT 8  
BE868556  
LOCUS 601444589F1 NIH\_MGC\_65 Homo sapiens cDNA clone IMAGE:3848374 5',  
DEFINITION mRNA sequence.  
ACCESSION BE868556  
VERSION BE868556.1 GI:10317332  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 915)  
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapsb@mail.nih.gov](mailto:cgapsb@mail.nih.gov)  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM9564 row: b column: 23  
High quality sequence stop: 693.  
Location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3848374"  
/tissue\_type="adenocarcinoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC\_65"  
/note="Organ: colon; Vector: PCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.8 kb. Library constructed by Life Technologies."

ORIGIN  
Query Match 73.5%; Score 681; DB 2; Length 915;  
Best Local Similarity 92.6%; Pred. No. 6.2e-188;  
Matches 749; Conservative 0; Mismatches 55; Indels 5; Gaps 3;  
QY 86 GGGGAATGGGATGAACAAGATCTTGGCCGCTGTACATCGGCACTTCAAGATGCGAG 145  
Db 8 GGGGAATGGGATGAACAAGATCTTGGCCGCTGTACATCGGCACTTCAAGATGCGAG 67  
QY 146 AGACGCGGAACAATTTGAGCAAGAACAAAGGTGACACATATTTCTGTCTCCACGATGTC 205  
Db 68 AGACGCGGAACAATTTGAGCAAGAACAAAGGTGACACATATTTCTGTCTCCACGATGTC 127



206 CAGGCTATGTTGGAGGAGTTAAATACCTGTGCATCCAGCAGCGGATTCACCATCTCA 265  
Db |||||  
128 CAGGCTATGTTGGAGGAGTTAAATACCTGTGCATCCAGCAGCGGATTCACCATCTCA 187  
Qy |||||  
266 AAACCTGACAGACATTTCAAAGAAAGTATTAATTCATTACAGAGTCGGGCTCCGGG 325  
Db |||||  
188 AAACCTGACAGACATTTCAAAGAAAGTATTAATTCATTACAGAGTCGGGCTCCGGG 247  
Qy |||||  
326 TGAGAGTCCTGTTGTACACTGCTCGCGGGGTCTCCAGGAGCGTGACACTGGTGATCGC 385  
Db |||||  
248 TGAGAGTCCTGTTGTACACTGCTCGCGGGGTCTCCAGGAGCGTGACACTGGTGATCGC 307  
Qy |||||  
386 ATACATCATGACCGCTCACTGACTTTGGCTGGGAGGATCCCTGCACACCGTCGCTGTGG 445  
Db |||||  
308 ATACATCATGACCGCTCACTGACTTTGGCTGGGAGGATCCCTGCACACCGTCGCTGTGG 367  
Qy |||||  
446 GAGATCCTGTGCCAACCCACCGTGGCTTCAGAGACAGCTCCAGGAGTTTGAGAAGCA 505  
Db |||||  
368 GAGATCCTGTGCCAACCCACCGTGGCTTCAGAGACAGCTCCAGGAGTTTGAGAAGCA 427  
Qy |||||  
506 TGAGGTCCATCAGTATCGSCAGTGGCTGAAGGAAGATATGGAGAGCGCTTTGCAGGA 565  
Db |||||  
428 TGAGGTCCATCAGTATCGSCAGTGGCTGAAGGAAGATATGGAGAGCGCTTTGCAGGA 487  
Qy |||||  
566 TGCAGAGAGCCAAACATTTCTGGCGCTCCAGGAATTTCTGAAGTTCTGGGCTTTCT 625  
Db |||||  
488 TGCAGAGAGCCAAACATTTCTGGCGCTCCAGGAATTTCTGAAGTTCTGGGCTTTCT 547  
Qy |||||  
626 CAGAGACTGTAATGTACTGAAGTTCTGAAGTTCTGAAGTTCTGAAGTTCTGAAGTTCT 685  
Db |||||  
548 CAGAGACTGTAATGTACTGAAGTTCTGAAGTTCTGAAGTTCTGAAGTTCTGAAGTTCT 607  
Qy |||||  
686 GTGCTGCCAAAGAAAGAACAGACATAGATTTAGTATCCAGTGTGATTTGTAACCTG 745  
Db |||||  
608 GTGCTGCCAAAGAAAGAACAGACATAGAG-TTAAAGTATCCAGTGTGATTTGTAACCTG 666  
Qy |||||  
746 TTTTTCATTGAAGCTGAATATATACGTAGTATCATTTTATTTGTGAAGAACTAAGGATATTC 805  
Db |||||  
667 GATTTCAATTTGAAGCTG-ATATATAGTGTAGTCAATGTACGTCGAGAACTCAGGATATTC 725  
Qy |||||  
806 TTTAGCAGAGAAATATTTTCCCTTATCCCACTGCTGTGGAGGTTTCTGTACCTCGC 865  
Db |||||  
726 TTAAGC---AGAGAAACATTTCCCTAATCCCACTGCTGTGGAGGTTCTGTACCTCGC 782  
Qy |||||  
866 TTGATGCTGTGAAGTCCCGGAGCT 894  
Db |||||  
783 TTGAGAGCTGTGAAGTCCCGGAGCTT 811

RESULT 9  
BG532390 665 bp mRNA linear EST 03-APR-2001  
LOCUS 602561902F1 NIH\_MGC\_61 Homo sapiens cDNA clone IMAGE:4699705 5',  
DEFINITION mRNA sequence.  
ACCESSION BG532390  
VERSION BG532390.1 GI:13523928  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 665)  
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
Tissue Procurement: ATCC  
cDNA Library Preparation: CLONETECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov  
Plate: L1CM532 row: c column: 02  
High quality sequence stop: 663.  
FEATURES  
Location/Qualifiers  
source  
1..665  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clones="IMAGE:4699705"  
/tissue\_type="embryonal carcinoma"  
/lab\_hosts="DH10B (TI phage-resistant)"  
/clone\_lib="NIH\_MGC\_61"  
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site: 1:  
SfiI (ggccattatggcc); Site 2: SfiI (ggccattatggcc);  
Double-stranded cDNA was prepared from cell line RNA. 5'  
and 3' adaptors were used in cloning as follows: 5'  
adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor  
sequence: 5'-ATTCTAGAGCGGCGGCACATG-dt(30)BN-3'  
(where B = A, C, or G and N = A, C, G, or T). Average  
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies  
contained inserts by PCR. This library was enriched for  
full-length clones and was constructed by Clontech  
Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC  
Library."  
ORIGIN  
Query Match. 70.6%; Score 653.8; DB 4; Length 665;  
Best Local Similarity 98.9%; Pred. No. 5.3e-180;  
Matches 658; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
Qy 56 GGGCGCTAGCGTTCGGCTTCAGCCACCATGGGGAATGGGATGAACAAGATCCTGCCCGG 115  
Db 1 GGGCGCTAGCGTTCGGCTTCAGCCACCATGGGGAATGGGATGAACAAGATCCTGCCCGG 60  
Qy 116 CCTGTACATCGGCAACTTCAAAGATGCGAGACGCGGAAACAATTGAGCAAGACAAAGT 175  
Db 61 CCTGTACATCGGCAACTTCAAAGATGCGAGACGCGGAAACAATTGAGCAAGACAAAGT 120  
Qy 176 GACACATATCTGTCTGTCCACGATAGTCCAGCGCTATGTTGGAGGGAGTTAAATACCT 235  
Db 121 GACACATATCTGTCTGTCCACGATAGTCCAGCGCTATGTTGGAGGGAGTTAAATACCT 180  
Qy 236 GTGCATCCAGCAGCGGATTCACCATCTCAAAACCTGACAAAGACATTTCAAAGAAAGTAT 295  
Db 181 GTGCATCCAGCAGCGGATTCACCATCTCAAAACCTGACAAAGACATTTCAAAGAAAGTAT 240  
Qy 296 TAAATTCATTCACGAGTCCCGGCTCCCGGTGAGAGTGCCTGTACATCGCTCGGCGG 355  
Db 241 TAAATTCATTCACGAGTCCCGGCTCCCGGTGAGAGTGCCTGTACATCGCTCGGCGG 300  
Qy 356 GGTCTCCAGAGCGGTGACACTGGTGATCGCATACATGACCGCTCACTGACTTTGGCTG 415  
Db 301 GGTCTCCAGAGCGGTGACACTGGTGATCGCACACATCATGACCGCTCACTGACTTTGGCTG 360  
Qy 416 GGAGATGCTCTGCACACCGTGTGTGGAGATCTGTGCCAACCCCAACCGTGGGCTT 475  
Db 361 GGAGATGCTCTGCACACCGTGTGTGGAGATCTGTGCCAACCCCAACCGTGGGCTT 420  
Qy 476 CCAGAGACAGCTCCAGGAGTTTGAGAGCATGAGGTCCATCAGTATCGGAGTGGCTGAA 535  
Db 421 CCAGAGACAGCTCCAGGAGTTTGAGAGCATGAGGTCCATCAGTATCGGAGTGGCTGAA 480  
Qy 536 GGAGATATGGAGAGCGCTTTGGAGGATCGAGAGAGCCAAACATTTCTGGCGG 595  
Db 481 GGAGATATGGAGAGCGCTTTGGAGGATCGAGAGAGCCAAACATTTCTGGCGG 540  
Qy 596 TCCAGGAATCTGAAGTTCTGGGCTTTCTCAGAAAGACTGTAAATGTACCTGAAGTTCTG 655  
Db 541 TCCAGGAATCTGAAGTTCTGGGCTTTCTCAGAAAGACTGTAAATGTACCTGAAGTTCTG 600  
Qy 656 AAATATGCAAAACCCGAGAGTTTAGGCTGTGCTGCCAAAGAAAGCAACATAGT 715  
Db 601 AAATATGCAAAACCCGAGAGTTTAGGCTGTGCTGCCAAAGAAAGCAACATAGT 660

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Qy      716 TTAAG 720
Db      661 TTAAG 665

RESULT 10
AV764304
LOCUS      AV764304 MDS Homo sapiens cDNA clone MDSBF09 5', mRNA linear EST 19-OCT-2000
DEFINITION AV764304
ACCESSION  AV764304
VERSION     AV764304.1 GI:10922152
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 694)
AUTHORS   Gu,J., Zhao,M., Huang,Q., Xu,X., Li,Y., Peng,Y., Song,H., Xiao,H.,
            Gu,Y., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z.,
            Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
            Lu,G., Yang,Y., Gao,G., Zhang,Q., Chen,S., Han,Z. and Chen,Z.
TITLE     Homo sapiens cDNA MDS clones
COMMENT   Unpublished (2000)
            Contact: Zeguang Han
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
            201203, P. R. China
            Tel: 86-21-50801919(ex.45)
            Fax: 86-21-50801922
            Email: hanzg@chgc.sh.cn
            This clone is available at CHGC in Shanghai.

FEATURES             source
            location/Qualifiers
            1..694
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="MDSBF09"
            /tissue_type="Bone marrow"
            /cell_type="CD34+ hematopoietic stem/progenitor cell"
            /lab_host="BM25.8"
            /clone_lib="MDS"
            /note="Vector: pTriplEx2; Site_1: sf1A; Site_2: sf1B"

ORIGIN
Query Match      69.6%; Score 644.2; DB 1; Length 694;
Best Local Similarity 96.3%; Pred. No. 3.5e-177;
Matches 658; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Qy      48 ACACGGCGGGCGGTAGCGTTCGCTTCAGCCACCATGGGGATGGGATGAACAAGATC 107
Db      1 ACACGGCGGGCGGTAGCGTTCGCTTCAGCCACCATGGGGATGGGATGAACAAGATC 60

Qy      108 CTGCCCGCGCTGTACATCGGCAACTTCAAAGATGCCAGACGCGGAACAATTGAGCAAG 167
Db      61 CTGCCCGCGCTGTACATCGGCAACTTCAAAGATGCCAGACGCGGAACAATTGAGCAAG 120

Qy      168 AACAGGTGACACATATTCTGTCTGTCCACGATAGTCCAGGCCCTATGTTGGAGGAGTT 227
Db      121 AACAGGTGACACATATTCTGTCTGTCTCCACGATAGTCCAGGCCCTATGTTGGAGGAGTT 180

Qy      228 AAATACCTGTGCATCCCGACGCGGATTCACCATCTCAAAACCTGACGACGACATTTCAA 287
Db      181 AAATACCTGTGCATCCCGACGCGGATTCACCATCTCAAAACCTGACGACGACATTTCAA 240

Qy      288 GAAAGTATTAAATTCATTACAGAGTCCGGCTCCGCGGTGAGAGCTGCTTGTGACATGC 347
Db      241 GAAAGTATTAAATTCATTACAGAGTCCGGCTCCGCGGTGAGAGCTGCTTGTGACATGC 300

Qy      348 CTGGCCGGGGTCTCCAGAGCGGTGACATCTGTTGATGCGATACATCATGACCGCTCACTGC 407
Db      301 CTGGCCGGGGTCTCCAGAGCGGTGACATCTGTTGATGCGATACATCATGACCGCTCACTGC 360

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Qy      408 TTTGGCTGGGAGGATGCCCTGCGACACCGTGCCTGGAGATCCTCTGCCAACCCCAAC 467
Db      361 TTTGGCTGNGAGGATGCCCTGCGACACCGTGCCTGGAGATCCTCTGCCAACCCCAAC 420

Qy      468 GTGGGCTTCCAGAGACAGACTCCAGGAGTTTGAGAAGCATGAGGTCCATCAGTATCGGCAG 527
Db      421 GTGGGCTTCCAGAGACAGACTCCAGGAGTTTGAGAAGCATGAGGTCCATCAGTATCGGCAG 480

Qy      528 TGGCTGAAGGAAGATATGAGAGAGAGCCCTTTGAGAGATGAGGTCCATCAGTATCGGCAG 587
Db      481 TGGCTGAAGGAAGATATGAGAGAGAGCCCTTTGAGAGATGAGGTCCATCAGTATCGGCAG 540

Qy      588 CTGGCCGCTCCAGCAATTTCTGAAGTTCTGGGCTTTCTCAGAGACTGTAATGACCTGA 647
Db      541 CTGGCCGCTTCAGGAATTTCTGAAGTTCTGGGCTTTCTCAGAGACTGTAATGACCTGA 600

Qy      648 AGTTTCTGAATAATATGCAAAACCCGACAGATTTAGGCTGGTCTGCCAAAAGAAAAGCAA 707
Db      601 AGTTTCTGAATAATATGCAAAACCCGACAGATTTAGGCTGGTCTGCCAAAAGAAAAGCAA 660

Qy      708 CATAGAGTTTAAGTATCCAGTAG 730
Db      661 GAGTTTGTATCAGTAGTATTG 683

RESULT 11
CD693732
LOCUS      CD693732 human nasopharynx Homo sapiens cDNA, mRNA linear EST 25-JUN-2003
DEFINITION CD693732
ACCESSION  CD693732
VERSION     CD693732.1 GI:32217678
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 655)
AUTHORS   Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
            Zeng,Y.-X.
TITLE     Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL    Unpublished (2003)
COMMENT    Contact: Yixin Zeng
            Cancer Center
            Sun Yat-sen University
            651 Dongfeng Road East, Guangzhou 510060, China
            Tel: 86-1380-9770-743
            Fax: 86-20-8775-4506
            Email: yxzeng@gzsums.edu.cn.

FEATURES             source
            location/Qualifiers
            1..655
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            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /tissue_type="normal nasopharynx"
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            /note="ESTs generated from a normal nasopharynx cDNA
            library from southern Chinese"

ORIGIN
Query Match      67.2%; Score 622.4; DB 6; Length 655;
Best Local Similarity 99.8%; Pred. No. 8.6e-171;
Matches 623; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      77 AGCCACCATGGGAATGGGATGAACAAGATCCTGCCCGGCTGTGATCGGCAACTTCAA 136
Db      32 AGCCACCATGGGAATGGGATGAACAAGATCCTGCCCGGCTGTGATCGGCAACTTCAA 91

Qy      137 AGATGCCAGAGACGCGGAACAATTGACAGAACAAAGTGCACATATTTCTGTGTGCTCA 196
Db      92 AGATGCCAGAGACGCGGAACAATTGACAGAACAAAGTGCACATATTTCTGTGTGCTCA 151

Qy      197 CGATAGTGCAGGCGCTATGTTGGAGGAGTTAAATACCTGTGATCCAGCAGCGGATTC 256

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Db 152 CGATAGTCCAGGCGCTATGTTGGAGGAGTTAAATACCTGTGCATCCAGCAGCGGATTC 211  
QY 257 ACCATCTCAAAACCTGCAAGACATTTCAAGAAAGTATTAAATTCATTCACAGAGTCCG 316  
Db 212 ACCATCTCAAAACCTGCAAGACATTTCAAGAAAGTATTAAATTCATTCACAGAGTCCG 271  
QY 317 GCTCCGCGGTGAGAGTGCCTTTGTACACTGCTGCGCGGGGTCTCCAGGAGCGTGACACT 376  
Db 272 GCTCCGCGGTGAGAGTGCCTTTGTACACTGCTGCGCGGGGTCTCCAGGAGCGTGACACT 331  
QY 377 GGTGATCGCATACATCATGACCGTCACTGACTTTGGCTGGGAGATGCCCTGCACACGT 436  
Db 332 GGTGATCGCATACATCATGACCGTCACTGACTTTGGCTGGGAGATGCCCTGCACACCGT 391  
QY 437 GCGTGTGGGAGATCCTGTGTCACCAACCCCAACCGTGGCTTCCAGAGACAGACTCCAGGAGTT 496  
Db 392 GCGTGTGGGAGATCCTGTGTCACCAACCCCAACCGTGGCTTCCAGAGACAGACTCCAGGAGTT 451  
QY 497 TGAGAAGCATGAGTCCATCATGATTCGCGAGTGGCTGAAGGAAGATATGGAGAGAGCCC 556  
Db 452 TGAGAAGCATGAGTCCATCATGATTCGCGAGTGGCTGAAGGAAGATATGGAGAGAGCCC 511  
QY 557 TTTGCGAGTGCAGAGAGCCAAACATTTCTGCGCGCTCCAGGAATTTGAAAGTTCTG 616  
Db 512 TTTGCGAGTGCAGAGAGCCAAACATTTCTGCGCGCTCCAGGAATTTGAAAGTTCTG 571  
QY 617 GGCCTTTCTCAGAGACTGTAATCTGACCTGAAGTTTCTGAAATATTGCAAAACCCAGAG 676  
Db 572 GGCCTTTCTCAGAGACTGTAATCTGACCTGAAGTTTCTGAAATATTGCAAAACCCAGAG 631  
QY 677 TTTAGGCTGGTGTGCCAAAAGA 700  
Db 632 TTTAGGCTGGTGTGCCAAAAGA 655

RESULT 12  
CB995799 819 bp mRNA linear EST 01-MAY-2003  
LOCUS AGENCOURT\_13684680 NIH\_MGC\_148 Homo sapiens cDNA clone  
DEFINITION IMAGE:30332322 5', mRNA sequence.  
CB995799  
VERSION CB995799.1 GI:30290223  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 819)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Dr. Stefan Hansson  
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help  
and advice from Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: NDAM349 row: c column: 19  
High quality sequence stop: 528.  
Location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
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/tissue\_type="pre-eclampsia placenta"  
/lab\_host="DH10B Tona"  
/clone\_lib="NIH\_MGC\_148"  
/note="Organ: placenta; Vector: pBluescriptR; site\_1:  
source

all-XhoI; Site 2: BamH; Library is oligo-dT primed and  
directionally cloned using primer  
5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert  
size 2.3 kb and normalized to 50x. This is a primary  
library enriched for full-length clones and constructed  
using the Cap-trapper method (Carninci, in preparation).  
Library constructed by M. Brownstein (NHGRI,  
National Institutes of Health). Note: this is a NIH\_MGC  
Library."

## ORIGIN

Query Match 65.6%; Score 607; DB 6; Length 819;  
Best Local Similarity 96.7%; Pred. No. 3e-166;  
Matches 641; Conservative 0; Mismatches 20; Indels 2; Gaps 2;  
QY 42 GCGACACACGCGCGCGCTAGCGTTCCGCTTCAGCCACCATGGGGAATGGGATGAAC 101  
Db 5 GCGAGTGACAGCGGTAGAACCCAGCGTTCGCTTCAGCCACCATGGGGAATGGGATGAAC 64  
QY 102 AAGATCTGCGCGCGCGCTGTACATCGGCAACTTCAAAGATGCCAGAGACGCCGAAACAATTG 161  
Db 65 AAGATCTGCGCGCGCGCTGTACATCGGCAACTTCAAAGATGCCAGAGACGCCGAAACAATTG 124  
QY 162 AGCAAGAAACAGGTGACACATATTTCTGTGTCCACGATAGTCCAGGCTTATGTTGAG 221  
Db 125 AGCAAGAAACAGGTGACACATATTTCTGTGTCCACGATAGTCCAGGCTTATGTTGAG 184  
QY 222 GGAGTTAAATACCTGTCATCCAGCAGCGGATTCACCATCTCAAAACCTGACAGACAT 281  
Db 185 GGAGTTAAATACCTGTCATCCAGCAGCGGATTCACCATCTCAAAACCTGACAGACAT 244  
QY 282 TTCAAGAAAGTATTAAATTCATTTCAGAGTCCCGGCTCCGCGGTGAGAGCTGCTTCTGA 341  
Db 245 TTCAAGAAAGTATTAAATTCATTTCAGAGTCCCGGCTCCGCGGTGAGAGCTGCTTCTGA 304  
QY 342 CACTGCTGCGCGCGGCTTCCAGGAGCGTGACACTGGTGTGATCGCATACATCATGACCGTC 401  
Db 305 CACTGCTGCGCGGCTTCCAGGAGCGTGACACTGGTGTGATCGCATACATCATGACCGTC 364  
QY 402 ACTGACTTTGGCTGGGAGGATGCCCTGCACACCGTGGTGGGAGATCTCTGTGCCAAC 461  
Db 365 ACTGACTTTGGCT--GGAGGATGCCCTGCACACCGTGGTGGGAGATCTCTGTGCCAAC 423  
QY 462 CCACACTGGCTTCCAGAGACAGCTCCAGGAGTTTCAGAGAGTTCAGAGTCCATCAGTAT 521  
Db 424 CCACACTGGCTTCCAGAGACAGCTCCAGGAGTTTCAGAGAGTTCAGAGTCCATCAGTAT 483  
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QY 582 AACATTCGCGCGCTCCAGGAATTCGAAGTTCGGGCTTTCTCAGAGACTGTAATGT 641  
Db 544 AACATTCGCGCGCTCCGGGAATTTCTGAAGTTCGGGCTTTCTCAGAGACTGTAATGT 603  
QY 642 ACCT-GAAGTTTCTGAATATTGCAAAACCCAGAGTTTAGGCTGGTCCCAAAAAGA 700  
Db 604 ACCTGAAGTTTCTGAATATTGCAAAACCCAGAGTTTAGGCTGGTCCCAAAAAGA 663  
QY 701 AAA 703  
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RESULT 13  
CA453928  
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DEFINITION mRNA sequence.  
CA453928  
ACCESSION CA453928.1 GI:24903167  
VERSION  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 930)  
 NIH-MGC http://mgi.nci.nih.gov/  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-rcmail.nih.gov  
 Tissue Procurement: Kristi A. Egland, Ira Pastan  
 cDNA Library Preparation: Invitrogen Corp  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: L14M14275 row: b column: 15  
 High quality sequence stop: 658.  
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 /clone="IWAGS:6718575"  
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 /lab\_host="EMDH10B"  
 /clone\_lib="MAPCL"  
 /note="Vector: pCMV-SPORT6; Site 1: EcoRV; Site 2: Not I; Subtracted with brain, liver, lung, kidney and muscle. Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold. Kristi A. Egland, James J. Vincent, Robert Strausberg, Bungkook Lee & Ira Pastan. Discovery of new breast cancer genes encoding membrane and secreted proteins. Manuscript submitted."  
 ORIGIN  
 Query Match 62.9%; Score 582.4; DB 6; Length 930;  
 Best Local Similarity 93.8%; Pred. No. 5.1e-159;  
 Matches 640; Conservative 0; Mismatches 36; Indels 6; Gaps 3;  
 QY 80 CACATCGGGAATGGATGACAGATCTTGGCCGGCTGTACATCGGCAACTTCAAAGA 139  
 DB 191 CGCGTGGCCATGTGACGCGCTACATCTGCGCGGCTGTACATCGGCAACTTCAAAGA 250  
 QY 140 TGGCAGAGACGCGGAACAATTGAGCAAGAAACAAGGTGACACATATCTGTCTGCCACGA 199  
 DB 251 TGGCAGAGACGCGGAACAATTGAGCAAGAAACAAGGTGACACATATCTGTCTGCCACGA 310  
 QY 200 TAGTCCAGCGCTATGTTGGAGGAGTTAAATACCTGTGTATCCACGCGGATTCACC 259  
 DB 311 TAGTCCAGCGCTATGTTGGAGGAGTTAAATACCTGTGTATCCACGCGGATTCACC 370  
 QY 260 ATCTCAAACTGACAGACATTTCAAGAAAGTATTAATTCATTCACGAGTCCGGCT 319  
 DB 371 ATCTCAAACTGACAGACATTTCAAGAAAGTATTAATTCATTCACGAGTCCGGCT 430  
 QY 320 CCGCGGTGAGAGCTGCTTGTACACTGCTGCGCGGCTTCCAGGAGCGTGACACTGGT 379  
 DB 431 CCGCGGTGAGAGCTGCTTGTACACTGCTGCGCGGCTTCCAGGAGCGTGACACTGGT 490  
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 DB 491 GATGCGCATACATGACCGTCACTGACTTGGCTGGAGAGATGCCCTGCACACCGGTGG 550  
 QY 440 TGCTGGGAGATCCGTGCGCAACCCACGCTGGCTCCAGAGACAGCTCCAGGATTTGA 499  
 DB 551 TGCTGGGAGATCCGTGCGCAACCCACGCTGGCTCCAGAGACAGCTCCAGGATTTGA 610  
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 DB 611 GAAGCATGAGGTCCATCAGTATCGGAGTGGCTGAAGGAAAGATATATGAGAGAGCCCTTT 670

QY 560 GCAGGATGCAGAGAACCCAAAACATTCTGGCCGCTCAGGAAATCTGAAGTCTGGG- 618  
 DB 671 GCAGGATGCAGAGAACCCAAAACATTCTGGCCGCTCAGGAAATCTGAAGTCTGGG- 730  
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 DB 791 TAAGCTGGTGCTGCCAAAAGAAAAGCAACATAGAGTTTAAAGTATCCAGTAGAAGAA 850  
 QY 734 TTGTAAACTTGTGTTTTCATT 755  
 DB 851 TTGCTAAACTTGTGTTTTCATT 872  
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 DEFINITION mRNA sequence.  
 ACCESSION BG545679 GI:13544344  
 VERSION BG545679  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 751)  
 NIH-MGC http://mgi.nci.nih.gov/  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-rcmail.nih.gov  
 Tissue Procurement: CLONTECH Laboratories, Inc.  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: L14M1535 row: j column: 11  
 High quality sequence stop: 680.  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:4701034"  
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 /clone\_lib="NIH\_MGC\_77"  
 /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcgctcgcc); Site 2: SfiI (ggcgatattggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGCGCGGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."  
 ORIGIN  
 Query Match 61.5%; Score 569.4; DB 4; Length 751;  
 Best Local Similarity 99.7%; Pred. No. 3.1e-155;  
 Matches 581; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
 QY 10 TCCTCTCTCTGTAACATGCTAGTGGCTCGCCTCGCACCAACACGCGCGGCGCTAGGTT 69  
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Qy 70 CGCCTTCAGCCACCATGGGGAATGGGATGAACAAGATCTCTCCCGGCTGTACATCGGCA 129  
Db 62 CGCCTTCAGCCACCATGGGGAATGGGATGAACAAGATCTCTCCCGGCTGTACATCGGCA 121  
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Qy 189 TCTGTCCACCATAGTGCAGCGCTTATGTTGGAGGAGTTAAATACCTGTGATCCAGCA 248  
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Qy 309 GAGTGCCTGCTCCCGGTGAGAGTGCCTGTGTACACTGCTGGCGGGGTCTCCAGGAGC 368  
Db 302 GAGTGCCTGCTCCCGGTGAGAGTGCCTGTGTACACTGCTGGCGGGGTCTCCAGGAGC 361  
Qy 369 GTGACACTGGTGATCGCATACATGACCGTCACTGACTTTGGCTGGAGGATGCCCTG 428  
Db 362 GTGACACTGGTGATCGCATACATGACCGTCACTGACTTTGGCTGGAGGATGCCCTG 421  
Qy 429 CACACCGTGGTGTGGGAGATCTGTGCCAACCCCAACGCTGGGCTTCCAGAGACAGCTC 488  
Db 422 CACACCGTGGTGTGGGAGATCTGTGCCAACCCCAACGCTGGGCTTCCAGAGACAGCTC 481  
Qy 489 CAGAGTTTGAGAGCATAGAGTCCATCAGTATCGGAGTGGCTGGAAGGAAGATATGGA 548  
Db 482 CAGAGTTTGAGAGCATAGAGTCCATCAGTATCGGAGTGGCTGGAAGGAAGATATGGA 541  
Qy 549 GAGAGCCCTTTGCAAGGATGCAGAGAGAGCCAAACCAATTCCTGG 591  
Db 542 GAGAGCCCTTTGCAAGGATGCAGAGAGAGCCAAACCAATTCCTGG 584

## RESULT 15

CN394735 712 bp mRNA linear EST 16-MAY-2004  
LOCUS 17000600186907 GRN\_PRENEU Homo sapiens cDNA 5', mRNA sequence.  
CN394735

## DEFINITION

CN394735

## ACCESSION

CN394735.1

## VERSION

GI:47382330

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

## REFERENCE

1 (bases 1 to 712)

## AUTHORS

Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,  
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,  
Lebkowski, J. and Stanton, L.W.

## TITLE

Transcriptome characterization elucidates signaling networks that  
control human ES cell growth and differentiation

## JOURNAL

Nat. Biotechnol. 22 (6), 707-716 (2004)

## COMMENT

Contact: Brandenberger R  
Regenerative Medicine  
Geron Corporation  
230 Constitution Drive, Menlo Park, CA 94025, USA  
Tel: 650 473 8658  
Fax: 650 473 7760  
Email: rbrandenberger@geron.com

## FEATURES

Location/Qualifiers

1..712

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/tissue\_type="embryonic stem cell, retinoic acid and  
mitogen-treated hES cell line H7"

/clone\_lib="GRN\_PRENEU"

/note="oligo dt primed, full-length enriched cDNA library  
from hES cell line H7 (p29) maintained in feeder-free

conditions. Embryoid bodies were generated in the presence  
of all-trans retinoic and mitogens."

ORIGIN  
Query Match 61.1%; Score 566; DB 7; Length 712;  
Best Local Similarity 100.0%; Pred. NO. 3e-154;  
Matches 566; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Qy 146 AGACGCGGAACAATTGAGCAAGAACAAAGGTGACACATATTCTGTCTCCACGATAGTGC 205  
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Qy 206 CAGGCTTATGTTGGAGGAGTTAAATACCTGTGTCATCCAGCAGCGGATTCACCATCTCA 265  
Db 181 CAGGCTTATGTTGGAGGAGTTAAATACCTGTGTCATCCAGCAGCGGATTCACCATCTCA 240  
Qy 266 AAACCTGACAAAGACATTTCAAGAAAGTATTAATTCATTCAAGTCCCGCTCCGCGG 325  
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Db 301 TGAGAGTCCCTGTGTACACTGCTGGCGGGGTCTCCAGAGCGTGACACTGGTGATCGC 360  
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Db 361 ATACATCATGACCGTCACTGACTTTGGCTGGAGGATGCCCTGCACACCGTGGCTGG 420  
Qy 446 GAGATCCTGTGCCAACCCCAACGTTGGCTTCCAGAGACAGCTCCAGGAGTTTGAGAAGCA 505  
Db 421 GAGATCCTGTGCCAACCCCAACGTTGGCTTCCAGAGACAGCTCCAGGAGTTTGAGAAGCA 480  
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Qy 566 TGCAGAGAGAGCCAAACCAATTCCTGG 591  
Db 541 TGCAGAGAGAGCCAAACCAATTCCTGG 566

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Job time : 3738 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

# OM nucleic - nucleic search, using sw model

Run on: July 21, 2005, 02:03:59 ; Search time 613 seconds  
(without alignments)  
8942.383 Million cell updates/sec

Title: US-10-658-661-1

Perfect score: 926

Sequence: 1 cccgcgcgtctctctcct.....ttgtgggtggttcgctgcgc 926

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq\_16Dec04:\*

1: geneseqn1980s:\*

2: geneseqn1990s:\*

3: geneseqn2000s:\*

4: geneseqn2001as:\*

5: geneseqn2001bs:\*

6: geneseqn2002as:\*

7: geneseqn2002bs:\*

8: geneseqn2003as:\*

9: geneseqn2003bs:\*

10: geneseqn2003cs:\*

11: geneseqn2003ds:\*

12: geneseqn2004as:\*

13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	926	100.0	926	4	Aaf32191 Human dua
3	926	100.0	926	10	ACC69509 Human DSP
4	926	100.0	926	12	ADN75953 Human sig
C 5	924	99.8	1187	4	AAS41391
C 6	924	99.8	1187	4	AAS43495
C 7	924	99.8	1187	10	ADC46153
8	923.6	99.7	1187	6	ABL90844 Human pol
9	922.8	99.7	1379	4	AAF63568 Human pho
10	922.8	99.7	1520	8	ACC83479 Human mlt
11	922.8	99.7	1520	10	ADD89786 Human MKP
12	922.8	99.7	1520	13	ADP25000 PRO poly
13	921.2	99.5	1290	3	AAZ46164 cDNA sequ
14	894.2	96.6	1161	5	ABV28356 Human pro
15	894.2	96.6	1161	5	ABV22541 Human pro
16	875.8	94.6	910	4	AAS34867 cDNA enco
17	875.8	94.6	910	10	ADC46025 Human neo
18	800.8	86.5	875	3	ACC63800 Human dua
19	623.4	67.3	625	4	AA164795 Human MAP
20	589.4	63.7	1218	5	AAF86152 Human JNK

## ALIGNMENTS

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AAF29601  
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AC AAF29601;

XX  
DT 06-APR-2001 (first entry)

XX  
DE Human DSP-3 CDNA.

XX  
KW Human; DSP-3; cytostatic; immunosuppressive; antiallergic;  
KW dual specificity phosphatase-3; cell proliferation; metabolic diseases;  
KW Duchenne muscular dystrophy; cancer; graft-versus-host disease;  
KW autoimmune disease; allergy; ss.

XX  
OS Homo sapiens.

XX  
PN WO200102582-A1.

XX  
PD 11-JAN-2001.

XX  
PF 29-JUN-2000; 2000WO-US018207.

XX  
PR 02-JUL-1999; 99US-0142338P.

XX  
PR 07-APR-2000; 2000WO-US009185.

XX  
PR 20-APR-2000; 2000WO-US010868.

XX  
PA (CBPT-) CBPTV INC.

XX  
PI Lucie RM, Wei B;

XX  
DR WPI; 2001-138149/14.

XX  
DR P-FSDB; AAB66431.

XX  
PT New dual-specificity phosphatase (DSP)-3 and DSP-3 alternate form  
PT polypeptides, useful for identifying modulators DSP-3 or DSP-3 alternate  
PT form activity, especially for treating e.g. cancer, autoimmune diseases  
PT or allergies.

XX  
PS Claim 7; Fig 1; 86pp; English.

XX  
CC The present sequence is given in a specification providing human dual  
CC specificity phosphatase-3 (DSP-3) and a murine DSP-3 variant polypeptide.

21 563.2 60.8 1067 4 AAF63565  
22 555 59.9 555 4 AAF29612  
23 488 52.7 2835 10 ADB63347  
24 479.6 51.8 2735 4 AAS41048  
25 469.2 50.7 2368 4 AAS41588  
26 421.2 45.5 687 4 AAF29608  
27 418.6 45.2 3010 5 AAF86153  
28 375.4 40.5 2420 6 ABZ35370  
29 334.4 36.1 3824 13 ADR06882  
30 274.2 29.6 555 12 ACH76515  
31 270.4 29.2 279 6 ABL70917  
32 200.8 21.7 867 10 ACC69512  
33 200.8 21.7 1160 6 AAD36481  
34 200.8 21.7 1160 10 ACC69513  
35 199.2 21.5 833 10 ACC69495  
36 199.2 21.5 833 12 ADN75957  
37 199.2 21.5 833 12 ADN76005  
38 199.2 21.5 1325 6 ABK14477  
39 199.2 21.5 1326 4 AAD09498  
40 199.2 21.5 1326 10 ACC69510  
41 198.2 21.4 705 10 ACC69511  
42 197.6 21.3 1123 6 ADI16571  
43 197.6 21.3 1123 12 ADN42225  
44 191.2 20.6 289 3 AAC75779  
45 180.8 19.5 1045 10 ACC69492

Aaf63565 Murine ph  
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Adb63347 Human cDN  
Aas41048 cDNA enco  
Aas41588 cDNA enco  
Aaf29608 Murine DS  
Aaf86153 Murine JN  
Abz35370 Human gen  
Achr06882 Full leng  
Ach76515 Human gen  
Abl70917 Corn tab88  
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Aad36481 Human pro  
Acc69513 Human DSP  
Acc69495 Human dua  
Adn75957 Human sig  
Adn76005 Human DSP  
Abk14477 Human pro  
Aad09498 Human SGP  
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Adn42225 Human cDN  
Aac75779 Human ORF  
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Qy 841 TGCTGTGGAGTTTCTGTACCTCGCTTGGATGCTGTGAAGATCCCGGAGCCTTGGCG 900
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Db 901 ACTGCTTGTGGGTGGCTTGGCGCTC 926
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AC ACC69509;
XX ACC69509;
XX ACC69509;
DT 21-JUL-2003 (first entry)
DE Human DSP-3 polynucleotide sequence SEQ ID NO:34.
XX Human; dual-specificity phosphatase; DSP-18; enzyme; cytostatic;
KW immunosuppressive; antiallergic; MAP-kinase modulator; dephosphorylation;
KW signal transduction modulator; cell proliferation; cell differentiation;
KW cell survival; proliferative response; Duchenne muscular dystrophy;
KW cancer; graft-versus-host disease; autoimmune disease; allergy;
KW metabolic disease; abnormal cell growth; abnormal cell proliferation;
KW cell cycle abnormality; gene; ss.
OS Homo sapiens.
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XX WO2003025196-A2.
XX 27-MAR-2003.
XX 16-MAY-2002; 2002WO-US015906.
XX 16-MAY-2001; 2001US-0291476P.
XX (CBPT-) CEPTVR INC.
XX Luche RM, Wei B;
XX WPI; 2003-371819/35.
XX New DSP-18 dual-specificity phosphatases, useful for modulating cell
XX proliferation, differentiation or survival, or for identifying modulators
XX of DSP-18 activity for treating e.g. cancer or graft-versus-host disease
XX in a patient.
XX Example 5; Page 109-110; 113pp; English.
XX ACC69489 to ACC69495 encode the human dual-specificity phosphatases
XX designated DSP-18a to DSP-19f and prototypic DSP-18pr given in ABR43450
XX to ABR43456. DSP-18 proteins have the ability to dephosphorylate an
XX activated mitogen activated protein (MAP)-kinase. DSP-18 sequences have
XX cytosolic, immunosuppressive and antiallergic activities, and can be
XX used as modulators of MAP-kinases and signal transduction. The DSP-18
XX proteins can be used for identifying antibodies and other modulators
XX (particularly inhibitors) of DSP-18 activity. The DSP-18 proteins may be
XX used to modulate cell proliferation, cell differentiation and cell
XX survival, or to treat diseases associated with cell proliferation,
XX differentiation or survival. The DSP-18 proteins are especially useful
XX for stimulating dephosphorylation of DSP-18 substrates. A modulator of
XX DSP-18 activity can be used for modulating a proliferative response in a
XX cell, differentiation of a cell or survival of a cell; or for treating a
XX cancer, graft-versus-host disease, autoimmune diseases, allergies,
XX metabolic diseases, abnormal cell growth, abnormal cell proliferation, or
XX cell cycle abnormalities) associated with DSP-18 activity. The present
XX sequence represents a human DSP-3 polynucleotide sequence which is used
XX in an example from the present invention
XX SQ Sequence 926 BP; 233 A; 230 C; 242 G; 221 T; 0 U; 0 Other;
```

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Query Match 100.0%; Score 926; DB 10; Length 926;
Best Local Similarity 100.0%; Pred. No. 1.1e-263;
Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CCCCCCGGCTCCTCCTCCTGTAACATGTCATAGTGGCTGCGCACACACGCGCGGGGC 60
Qy 61 GCTAGCGTTGCGCTTCAGCCACCATGCGGGAATGGGATGAACAAGATCTGCGCGGCTGT 120
Db 61 GCTAGCGTTGCGCTTCAGCCACCATGCGGGAATGGGATGAACAAGATCTGCGCGGCTGT 120
Qy 121 ACATCGGCAACTTCAAGATGCCAGACGCGGGAACAAATTGAGCAAGAACAAAGGTGACAC 180
Db 121 ACATCGGCAACTTCAAGATGCCAGACGCGGGAACAAATTGAGCAAGAACAAAGGTGACAC 180
Qy 181 ATATTCTGTCTGTCCAGATAGTGCAGGCTATGTTGGAGGAGTTAAATACCTGTGCA 240
Db 181 ATATTCTGTCTGTCCAGATAGTGCAGGCTATGTTGGAGGAGTTAAATACCTGTGCA 240
Qy 241 TCCAGAGCGGATTCACCATCTCAAAACCTGACAGACATTTCAAGAAAGTATTAAAT 300
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Qy 301 TCATTTCAGAGTGCAGGCTCGCGGTGAGAGTGCCTGTGTACACTGCTGCGCGGGGTCT 360
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Db 722 TATCCAGTAGTGAATTTGAAACTTCTTTTTCATTGGAAGCTGAATATATACGTAGTCAATG 780  
QY 781 TTTATGTTGAGAACTAAGGATATCTTTTACGAAGAGAAAAATATTTTCCCTTATCCCCAC 840  
Db 782 TTTATGTTGAGAACTAAGGATATCTTTTACGAAGAGAAAAATATTTTCCCTTATCCCCAC 840  
QY 841 TGCTGTGAGGCTTTCTGTACCTCGCTTGGATCCCTGTAAGGATCCCGGAGCCTTGCGGC 900  
Db 842 TGCTGTGAGGCTTTCTGTACCTCGCTTGGATCCCTGTAAGGATCCCGGAGCCTTGCGGC 900  
QY 901 ACTGCTTGTGGGCTTGGCTTGGCGCTC 926  
Db 902 ACTGCTTGTGGGCTTGGCTTGGCGCTC 926

RESULT 5  
ID AAS41391/c  
AC AAS41391;  
DT 17-DEC-2001 (first entry)  
DE cDNA encoding novel human enzyme polypeptide #607.  
KW Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;  
KW ligase; hyperproliferative disorder; immunodeficiency disorder;  
KW autoimmune disorder; neurological disorder; metabolic disorder;  
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;  
KW blood-related disorder; infectious disorder; gene therapy; cytostatic;  
KW anti arthritic; nephrotropic; anticoagulant; ss.  
OS Homo sapiens.  
PN WO200155301-A2.  
XX 02-AUG-2001.  
XX 17-JAN-2001; 2001WO-US001239.  
PR 31-JAN-2000; 2000US-0179065P.  
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PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Barash SC, Ruben SM;  
XX  
XX WPI; 2001-465566/50.  
DR P-PSDB; AAU23521.  
XX  
PT Novel polypeptides and polynucleotides useful for diagnosing, preventing,  
PT treating neural, immune system, muscular, reproductive, pulmonary,  
PT cardiovascular, renal, proliferative disorders and cancerous diseases.  
XX  
PS Claim 4; SEQ ID NO 617; 1180pp; English.  
XX  
CC The present invention relates to the isolation of novel human enzyme  
CC polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences  
CC encoding them. The enzyme polypeptides of the invention may comprise the  
CC functional classes of oxidoreductases, transferases, hydrolases, lyases,  
CC isomerases or ligases. The sequences of the invention are useful in the  
CC diagnosis, treatment, prevention and/or prognosis of a wide range of  
CC disorders including hyperproliferative disorders (e.g. cancer),  
CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g.  
CC arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic  
CC disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma),  
CC cardiovascular disorders (e.g. atherosclerosis), blood-related disorders  
CC (e.g. haemophilia), reproductive disorders (e.g. infertility) and  
CC infectious disorders (e.g. Influenza). The polynucleotides of the  
CC invention can also be used in gene therapy. AA540785-AA541684 represent  
CC cDNA sequences encoding for the novel human enzyme polypeptides of the  
CC invention. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1187 BP; 288 A; 302 C; 290 G; 306 T; 0 U; 1 Other;

Query Match 99.8%; Score 924; DB 4; Length 1187;  
Best Local Similarity 99.8%; Pred. No. 5e-263;  
Matches 924; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db |||||  
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Qy 421 ATGCCCTGCACACCGTCCGTGGGAGATCCCTGTGCAACCCCAACCGTGGGCTTCCAGA 480  
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316 TGTGTTGGAGGTTTCTGTACTGCTGGATGCTGTGAAGATCCCGGAGCCTTGGCGC 257  
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RESULT 6  
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ID AAS34995 standard; cDNA; 1187 BP.  
XX  
AC AAS34995;  
XX  
DT 04-DEC-2001 (first entry)  
XX

DE cDNA encoding novel human neoplastic disease associated polypeptide #229.  
XX Human; neoplastic disease associated polypeptide; cancer; gene therapy;  
KW hyperproliferative disorder; neural disorder; immune system disorder;  
KW muscular disorder; reproductive disorder; gastrointestinal disorder;  
KW pulmonary disorder; cardiovascular disorder; renal disorder;  
KW neuroprotective; cytostatic; anti inflammatory; vasotropic; ss.  
OS Homo sapiens.  
XX  
XX WO200155163-A1.  
XX  
XX PD 02-AUG-2001.  
XX  
XX PF 17-JAN-2001; 2001WO-US001358.  
XX  
XX PR 31-JAN-2000; 2000US-0179065P.  
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PR 05-DEC-2000; 2000US-0251030P.  
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 PR 14-AUG-2000; 2000US-0224519P.  
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 PR 14-AUG-2000; 2000US-0225214P.  
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 PR 22-AUG-2000; 2000US-0227182P.  
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 PR 01-SEP-2000; 2000US-0229287P.  
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 PR 01-SEP-2000; 2000US-0229344P.  
 PR 01-SEP-2000; 2000US-0229345P.  
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 PR 08-SEP-2000; 2000US-0231244P.  
 PR 08-SEP-2000; 2000US-0231413P.  
 PR 08-SEP-2000; 2000US-0231414P.  
 PR 08-SEP-2000; 2000US-0232080P.  
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 PR 12-SEP-2000; 2000US-0231988P.  
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 PR 14-SEP-2000; 2000US-0232398P.  
 PR 14-SEP-2000; 2000US-0232399P.  
 PR 14-SEP-2000; 2000US-0232400P.  
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 PR 14-SEP-2000; 2000US-0233064P.  
 PR 14-SEP-2000; 2000US-0233065P.  
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 PR 21-SEP-2000; 2000US-0234274P.  
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 PR 25-SEP-2000; 2000US-0234998P.  
 PR 26-SEP-2000; 2000US-0235484P.  
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 PR 27-SEP-2000; 2000US-0235836P.  
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 PR 29-SEP-2000; 2000US-0236370P.  
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 PR 02-OCT-2000; 2000US-0237038P.  
 PR 02-OCT-2000; 2000US-0237039P.  
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 PR 13-OCT-2000; 2000US-0239937P.

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 PR 08-NOV-2000; 2000US-0246609P.  
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 PR 17-NOV-2000; 2000US-0249209P.  
 PR 17-NOV-2000; 2000US-0249210P.  
 PR 17-NOV-2000; 2000US-0249211P.  
 PR 17-NOV-2000; 2000US-0249212P.  
 PR 17-NOV-2000; 2000US-0249213P.  
 PR 17-NOV-2000; 2000US-0249214P.  
 PR 17-NOV-2000; 2000US-0249215P.  
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 PR 17-NOV-2000; 2000US-0249217P.  
 PR 17-NOV-2000; 2000US-0249218P.  
 PR 17-NOV-2000; 2000US-0249244P.  
 PR 17-NOV-2000; 2000US-0249245P.  
 PR 17-NOV-2000; 2000US-0249264P.  
 PR 17-NOV-2000; 2000US-0249265P.  
 PR 17-NOV-2000; 2000US-0249299P.  
 PR 17-NOV-2000; 2000US-0249300P.  
 PR 01-DEC-2000; 2000US-0250160P.  
 PR 01-DEC-2000; 2000US-0250351P.  
 PR 05-DEC-2000; 2000US-0251030P.  
 PR 05-DEC-2000; 2000US-0251988P.  
 PR 05-DEC-2000; 2000US-0256719P.  
 PR 06-DEC-2000; 2000US-0251479P.  
 PR 08-DEC-2000; 2000US-0251856P.  
 PR 08-DEC-2000; 2000US-0251868P.  
 PR 08-DEC-2000; 2000US-0251869P.  
 PR 08-DEC-2000; 2000US-0251989P.  
 PR 08-DEC-2000; 2000US-0251990P.  
 PR 11-DEC-2000; 2000US-0254097P.  
 PR 05-JAN-2001; 2001US-0259678P.  
 PR 17-JAN-2001; 2001US-00764854.

XX (HUMA-) HUMAN GENOME SCI INC.  
 XX PA  
 XX PI Rosen CA, Ruben SM, Barash SC;  
 XX PI WPI; 2003-786918/74.  
 XX DR P-PSDB; ADC46437.  
 XX DR  
 XX PT New isolated human neoplastic disease-associated polypeptides and  
 XX PT polynucleotides, useful for diagnosing, preventing, prognosticating or  
 XX PT treating medical conditions such as cancer, AIDS, diabetes or Parkinson's  
 XX PT disease.  
 XX PS Claim 1; SEQ ID NO 239; 302pp; English.  
 XX





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Db 437 ATATTCTGTCTGTCCACGATAGTCCAGGCCCTATGTTGGAGGGAGTTAAATACCTGTGCA 496
Qy 241 TCCACAGCAGCGGATTCAACATCTCTAAACCTGACAAAGACATTTCAAAGAAAAGTATTAAAT 300
Db 497 TCCACAGCAGCGGATTCAACATCTCTAAACCTGACAAAGACATTTCAAAGAAAAGTATTAAAT 556
Qy 301 TCATTACAGAGTGC CGGCTCCGCGGTGAGAGTGCCTTTGTACACTGCGCTGCGCGGTCT 360
Db 557 TCATTACAGAGTGC CGGCTCCGCGGTGAGAGTGCCTTTGTACACTGCGCTGCGCGGTCT 616
Qy 361 CCAGGAGCGTGACACTGGTGATCGCATACATCATGACCGTCACTGACTTTGGCTGGGAGG 420
Db 617 CCAGGAGCGTGACACTGGTGATCGCATACATCATGACCGTCACTGACTTTGGCTGGGAGG 676
Qy 421 ATGCCCTGCACACCGTGCCTGCGGTGAGAGATCTGTGCGCAACCCCAACCTGGGCTTCCAGA 480
Db 677 ATGCCCTGCACACCGTGCCTGCGGTGAGAGATCTGTGCGCAACCCCAACCTGGGCTTCCAGA 736
Qy 481 GACAGCTCCAGAGCTTTGAGAGCATGAGTGGTCCATCAGTATCGGAGTGGCTGAAGGAG 540
Db 737 GACAGCTCCAGAGCTTTGAGAGCATGAGTGGTCCATCAGTATCGGAGTGGCTGAAGGAG 796
Qy 541 AATATGAGAGAGCGCTTTGAGAGATGAGAGAGAGCCAAACCAATTTCTGGCGCTCCAG 600
Db 797 AATATGAGAGAGCGCTTTGAGAGATGAGAGAGAGCCAAACCAATTTCTGGCGCTCCAG 856
Qy 601 GAAATCTGAAGTCTGGGCTTTCTCAGAGACTGTAATGACTGTAAGTTTCTGAAATA 660
Db 857 GAAATCTGAAGTCTGGGCTTTCTCAGAGACTGTAATGACTGTAAGTTTCTGAAATA 916
Qy 661 TTGCAAAACCCAGAGTTTACGCTGGTCTGCCAAAGAAAGCAACATAGAGTTTAAAG 720
Db 917 TTGCAAAACCCAGAGTTTACGCTGGTCTGCCAAAGAAAGCAACATAGAGTTTAAAG 976
Qy 721 TATCAGTAGTCAATTTGTAACCTTTGTTTTTCAATTTGAAGCTGAAATATATAGTATCATG 780
Db 977 TATCAGTAGTCAATTTGTAACCTTTGTTTTTCAATTTGAAGCTGAAATATATAGTATCATG 1036
Qy 781 TTTATGTTGAGAACTAAGGATATTTTATGCAAGAGAAAATATTTTCCCTTTATCCCGAC 840
Db 1037 TTTATGTTGAGAACTAAGGATATTTTATGCAAGAGAAAATATTTTCCCTTTATCCCGAC 1096
Qy 841 TGCTGTGAGGTTTCTGTACCTCGCTGGATGCGCTGTAAGGATCCCGGAGCCTTGGCGC 900
Db 1097 TGCTGTGAGGTTTCTGTACCTCGCTGGATGCGCTGTAAGGATCCCGGAGCCTTGGCGC 1156
Qy 901 ACTGCTTGTGGTGGCTTGGCGCTC 926
Db 1157 ACTGCTTGTGGTGGCTTGGCGCTC 1182
```

RESULT 10  
ACC83479

ID ACC83479 standard; cDNA; 1520 BP.

XX ACC83479;

AC ACC83479;

DT 08-SEP-2003 (first entry)

XX Human mitogen-activated protein kinase phosphatase X (MKPX) cDNA.

DE Mitogen-activated protein kinase phosphatase X; MKPX; enzyme; human;  
KW cancer; vaccine; gene therapy; cytosolic; chromosome 6p25.3; gene; ss.

OS Homo sapiens.

XX Key Location/Qualifiers  
FH 449..1003  
CDS /\*tag= a

FT /product= "Human MKPX"

FT /note= "the CDS is also claimed in Claim 12"

XX PN W02003044161-A2.

XX 30-MAY-2003.  
PD 05-NOV-2002; 2002WO-US035312.  
XX 15-NOV-2001; 2001US-0331394P.  
XX (TULA-) TULARIK INC.  
XX Sin WC, Yang J;  
PI WPI; 2003-457600/43.  
DR P-PSDB; ABR42923.  
XX  
PT New isolated mitogen-activated protein kinase phosphatase X gene  
PT amplicon, useful for diagnosing, preventing and treating pre-cancerous  
PT lesions or cancer in a mammal, e.g. colon, prostate or ovarian cancer.  
XX  
PS Claim 12; Page 89; 90pp; English.

XX The present sequence, the coding portion of which is also claimed,  
CC encodes human mitogen-activated protein kinase phosphatase X (MKPX). MKPX  
CC is amplified and overexpressed in human cancers, including colon cancer,  
CC ovarian cancer and prostate cancer. The MKPX gene, its expressed protein  
CC products and antibodies can be used diagnostically or as targets for  
CC cancer therapy or vaccine. They are also used to identify compounds and  
CC reagents useful in cancer diagnosis, prevention and therapy, and for  
CC determining the efficacy of a therapeutic treatment regimen in a patient.  
CC A claimed method of blocking in vivo expression of the gene involves  
CC administering a vector encoding MKPX small interfering RNA (siRNA)

XX SQ Sequence 1520 BP; 348 A; 412 C; 431 G; 329 T; 0 U; 0 Other;

Query Match 99.7%; Score 922.8; DB 8; Length 1520;  
Best Local Similarity 99.8%; Pred. No. 1.3e-262;  
Matches 924; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCGCGCGCTCTCTCTCTCTGTAACATGCCATAGTGGCCCTGCCACACACGCGCGGGGC 60  
Db 366 CCGCGCGCTCTCTCTCTCTGTAACATGCCATAGTGGCCCTGCCACACACGCGCGGGGC 425  
Qy 61 GCTAGCGTTCCGCTTTCAGCCACCATGCGGAATGGATGAACAAGATCCTGCCCGGCTGT 120  
Db 426 GCTAGCGTTTCCGCTTTCAGCCACCATGCGGAATGGATGAACAAGATCCTGCCCGGCTGT 485  
Qy 121 ACATCGGCAACTTCAAAGATGCCAGAGACGCGGAACAATTTGAGCAAGAAACAAGTGACAC 180  
Db 486 ACATCGGCAACTTCAAAGATGCCAGAGACGCGGAACAATTTGAGCAAGAAACAAGTGACAC 545  
Qy 181 ATATTCTGTCTGTCCACGATAGTCCAGGCTTATGTTGGAGGGAGTTAAATACCTGTGCA 240  
Db 546 ATATTCTGTCTGTCCACGATAGTCCAGGCTTATGTTGGAGGGAGTTAAATACCTGTGCA 605  
Qy 241 TCCACAGCAGCGGATTCAACATCTCAAAACCTGACAAAGACATTTCAAAGAAAAGTATTAAAT 300  
Db 606 TCCACAGCAGCGGATTCAACATCTCAAAACCTGACAAAGACATTTCAAAGAAAAGTATTAAAT 665  
Qy 301 TCATTACAGAGTGC CGGCTCCGCGGTGAGAGTGCCTTTGTACACTGCGCTGCGCGGTCT 360  
Db 666 TCATTACAGAGTGC CGGCTCCGCGGTGAGAGTGCCTTTGTACACTGCGCTGCGCGGTCT 725  
Qy 361 CCAGGAGCGTGACACTGGTGATCGCATACATCATGACCGTCACTGACTTTGGCTGGGAGG 420  
Db 726 CCAGGAGCGTGACACTGGTGATCGCATACATCATGACCGTCACTGACTTTGGCTGGGAGG 785  
Qy 421 ATGCCCTGCACACCGTGCCTGCGGAGATCTCTGTGCCAAACCCCAACCTGGGCTTCCAGA 480  
Db 786 ATGCCCTGCACACCGTGCCTGCGGAGATCTCTGTGCCAAACCCCAACCTGGGCTTCCAGA 845  
Qy 481 GACAGCTCCAGGAGTTTGAAGAGCATGAGGTCCATCATAGTATCGGCAGTGGCTGAAGGAG 540  
Db 846 GACAGCTCCAGGAGTTTGAAGAGCATGAGGTCCATCATAGTATCGGCAGTGGCTGAAGGAG 905



Db 906 AATATGGAGAGCCCTTTGAGGATGACAGAGCCAGCAAAACATTTGCGCGCTCCAG 965  
Qy 601 GAATTCGAAGTTCTGGGCCCTTTCTCAGAGACTGTAAATGACCTGAAGTTTCTGAATA 660  
Db 966 GAAATCTGAAGTTCTGGGCCCTTTCTCAGAGACTGTAAATGACCTGAAGTTTCTGAATA 1025  
Qy 661 TTGCAAAACCCAGAGTTTACGCTGGTCTGCCAAAAGAAAGCAACATAGAGTTTAAAG 720  
Db 1026 TTGCAAAACCCAGAGTTTACGCTGGTCTGCCAAAAGAAAGCAACATAGAGTTTAAAG 1085  
Qy 721 TATCAGTAGTGAATTTGTAACCTTTCTTTTTCATTTGAAAGCTGCAATATATAGCTAGTCATG 780  
Db 1086 TATCAGTAGTGAATTTGTAACCTTTCTTTTTCATTTGAAAGCTGCAATATATAGCTAGTCATG 1145  
Qy 781 TTTATGTTGAGAACTAAGGATATCTTTTGAAGAGAGAAAATATTTTCCCTTATCCCCAC 840  
Db 1146 TTTATGTTGAGAACTAAGGATATCTTTTGAAGAGAGAAAATATTTTCCCTTATCCCCAC 1205  
Qy 841 TGCTGTGAGGTTTCTGTACCTCGCTTGGATGCTGTAAGGATCCCGGAGCCTTGCCGC 900  
Db 1206 TGCTGTGAGGTTTCTGTACCTCGCTTGGATGCTGTAAGGATCCCGGAGCCTTGCCGC 1265  
Qy 901 ACTGCTTTGTGGTGGCTTGGCGCTC 926  
Db 1266 ACTGCTTTGTGGTGGCTTGGCGCTC 1291

RESULT 12  
ID ADP25000 standard; cDNA; 1520 BP.  
AC ADP25000;  
XX  
XX  
XX 18-NOV-2004 (first entry)  
XX  
DE PRO polypeptide encoding cDNA SEQ ID NO:2178.  
XX  
XX ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic;  
KW immunosuppressive; osteopathic; antidiabetic; dermatological;  
KW antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory;  
KW gene therapy; immune system.  
XX  
OS Unidentified.  
XX  
FN WO2004041170-A2.  
XX  
XX 21-MAY-2004.  
XX  
PF 30-OCT-2003; 2003WO-US034312.  
XX  
PR 01-NOV-2002; 2002US-0423394P.  
XX  
PA (GETH ) GENENTECH INC.  
PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;  
PI Wu TD;  
XX  
XX WPI; 2004-419628/39.  
DR P-PSDB; ADP25001.  
XX  
PT New PRO polypeptides and polynucleotides, useful for treating e.g.  
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated  
PT renal disease, or demyelinating diseases of the central or peripheral  
PT nervous system.  
XX  
PS Claim 1; SEQ ID NO 2178; 2940pp; English.  
XX  
CC The invention relates to a novel isolated nucleic acid and the PRO  
CC polypeptide encoded by it. A protein of the invention has  
CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,  
CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,  
CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide  
CC of the invention may have a use in gene therapy. The PRO polypeptide, its

CC agonist, antagonist, or antibody that specifically binds to the  
CC polypeptide is useful for treating an immune related disorder such as  
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an  
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal  
CC disease, a demyelinating disease of the central or peripheral nervous  
CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,  
CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary  
CC disease, infectious or autoimmune chronic active hepatitis, primary  
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,  
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's  
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin  
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic  
CC disease, asthma, allergic rhinitis, atopic dermatitis, food  
CC hypersensitivity, urticaria, an immunologic disease of the lung,  
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity  
CC pneumonitis, a transplantation associated disease, graft rejection or  
CC graft-versus-host disease. The present sequence encodes a PRO protein of  
CC the invention.  
XX  
XX  
Qy Sequence 1520 BP; 348 A; 412 C; 431 G; 329 T; 0 U; 0 Other;  
Query Match 99.7%; Score 922.8; DB 13; Length 1520;  
Best Local Similarity 99.8%; Pred. No. 1.3e-262;  
Matches 924; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 CCCGCCGCTCTCTCCCTGTAACATGTCATAGTGGCCCTGGACACACGCGCGGGC 60  
Db 366 CCCGCCGCTCTCTCCCTGTAACATGTCATAGTGGCCCTGGACACACGCGCGGGC 425  
Qy 61 GCTAGCTTCGCTTCAGCCACCATGGGAAATGGGATGAACAAGATCCTGCGCGGCTGT 120  
Db 426 GCTAGCTTCGCTTCAGCCACCATGGGAAATGGGATGAACAAGATCCTGCGCGGCTGT 485  
Qy 121 ACATCGGCACTTCAAGATGCCAGAGCGGAGCAATTTGAGCAAGAAAGTGTACAC 180  
Db 486 ACATCGGCACTTCAAGATGCCAGAGCGGAGCAATTTGAGCAAGAAAGTGTACAC 545  
Qy 181 ATATTCTGTCTGTCCACGATAGTCCAGGCTATGTTGGAGGGAGTTAAATACCTGTGCA 240  
Db 546 ATATTCTGTCTGTCCACGATAGTCCAGGCTATGTTGGAGGGAGTTAAATACCTGTGCA 605  
Qy 241 TCCAGCAGCGGATTCACATCTCAAAACCTGACAGACATTTCAAAGAAGTATTAAT 300  
Db 606 TCCAGCAGCGGATTCACATCTCAAAACCTGACAGACATTTCAAAGAAGTATTAAT 665  
Qy 301 TCATTACAGAGTCCGGCTCCGGGTGAGAGCTGCCCTGTGTACACTGCTGCGCGGGTCT 360  
Db 666 TCATTACAGAGTCCGGCTCCGGGTGAGAGCTGCCCTGTGTACACTGCTGCGCGGGTCT 725  
Qy 361 CCAGGAGCTGACACTGCTGATGCATACATCATGACCGTCACTGACTTTGGCTGGGAGG 420  
Db 726 CCAGGAGCTGACACTGCTGATGCATACATCATGACCGTCACTGACTTTGGCTGGGAGG 785  
Qy 421 ATGCCCTGACACCGTGGCTGGGAGATCTGTGCAACCCCAACCGTGGGCTTCCAGA 480  
Db 786 ATGCCCTGACACCGTGGCTGGGAGATCTGTGCAACCCCAACCGTGGGCTTCCAGA 845  
Qy 481 GACAGCTCCAGGAGTTTGAAGCATGAGTCCATCAGTATCGGACGTGGCTGAAGGAAG 540  
Db 846 GACAGCTCCAGGAGTTTGAAGCATGAGTCCATCAGTATCGGACGTGGCTGAAGGAAG 905  
Qy 541 AATATGAGAGAGCCCTTTGCGAGGATGCAGAGAGCCAAAACATTTCTGCGCGCTCCAG 600  
Db 906 AATATGAGAGAGCCCTTTGCGAGGATGCAGAGAGCCAAAACATTTCTGCGCGCTCCAG 965  
Qy 601 GAATTCGAAGTTCTGGGCCCTTTCTCAGAGACTGTAAATGACCTGAAGTTTCTGAATA 660  
Db 966 GAATTCGAAGTTCTGGGCCCTTTCTCAGAGACTGTAAATGACCTGAAGTTTCTGAATA 1025  
Qy 661 TTGCAAAACCCAGAGTTTACGCTGGTCTGCCAAAAGAAAGCAACATAGAGTTTAAAG 720



Db 1026 TTGCAAAACCCAGAGTTTAGCTGGTGTGCTGCAAAAAGAAAGCAACATAGAGTTTAAG 1085  
Qy 721 TATCCAGTAGTGATTTGTAACCTGCTTTTCAATTTGAAGCTGAATATATAGTGTATG 780  
Db 1086 TATCCAGTAGTGATTTGTAACCTGCTTTTCAATTTGAAGCTGAATATATAGTGTATG 1145  
Qy 781 TTTATGTTGAGAACTAAGGATATCTTTAGCAAGAGAAAAATATTTTCCCTTATCCCCAC 840  
Db 1146 TTTATGTTGAGAACTAAGGATATCTTTAGCAAGAGAAAAATATTTTCCCTTATCCCCAC 1205  
Qy 841 TGCTGTGAGGTTTCTGACCTCGCTTGATGCGCTGTAAAGATCCCGGAGGCTTGCCTG 900  
Db 1206 TGCTGTGAGGTTTCTGACCTCGCTTGATGCGCTGTAAAGATCCCGGAGGCTTGCCTG 1265  
Qy 901 ACTGCTTTGTGGTGGCTTTGGCGCTC 926  
Db 1266 ACTGCTTTGTGGTGGCTTTGGCGCTC 1291

## RESULT 13

AAZ46164

ID AAZ46164 standard; cDNA; 1290 BP.

XX AAZ46164;

DT 16-MAY-2000 (first entry)

DE cDNA sequence encoding a human phosphorylation effector PHSP-27.  
XX Human; phosphorylation effector; PHSP; proliferative disorder;  
KW immune disorder; neuronal disorder; ss.  
OS Homo sapiens.

XX Key Location/Qualifiers

FH 238..792

CDS /\*tag= a

FT /\*product= "phosphorylation effector"

XX WO200006728-A2.

XX 10-FEB-2000.

XX 28-JUL-1999; 99WO-US017132.

XX 28-JUL-1998; 98US-0155213P.

PR 14-SEP-1998; 98US-0155196P.

PR 14-OCT-1998; 98US-0155239P.

PR 03-NOV-1998; 98US-0106889P.

PR 19-NOV-1998; 98US-0109093P.

PR 22-DEC-1998; 98US-0113796P.

PR 12-JAN-1999; 99US-0155233P.

XX (INCY-) INCYTE PHARM INC.

XX Hillman JL, Lal P, Tang YT, Corley NC, Guegler KJ, Baughn MR;

PI Patterson C, Bandman O, Au-Young J, Gorgone GA, Yue H, Azimzai Y;

PI Reddy R, Lu DAW, Shih LL;

XX WPI; 2000-183125/16.

DR P-PSDB; AAY68795.

PT New human phosphorylation effectors useful for the diagnosis, treatment  
PT and prevention of proliferative, immune and neuronal disorders.  
XX Claim 9; Page 139; 142pp; English.

XX AAZ46138-246168 encode human phosphorylation effectors (PHSP), designated

CC PHSP1-PHSP31 (the protein sequence for PHSP28 is not given in the

CC specification). The sequences were isolated from cDNA libraries prepared

CC from various human tissues. The PHSP proteins are useful for the

CC diagnosis, treatment and prevention of proliferative disorders, immune

CC disorders and neuronal disorders. The PHSP proteins form pharmaceutical  
CC compositions which useful for treating or preventing disorders associated  
CC with decreased PHSP expression/activity. PHSP antagonists are useful for  
CC treating or preventing disorders associated with increased PHSP  
CC expression/activity  
XX

SQ Sequence 1290 BP; 299 A; 341 C; 339 G; 311 T; 0 U; 0 Other;

Query Match 99.5%; Score 921.2; DB 3; Length 1290;

Best Local Similarity 99.7%; Pred. No. 3.5e-262;

Matches 923; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCGCGCTCCTCCTCCCTGTAACATGCCATAGTCGCCCTGCGACACACGCGCGGCG 60

Db 155 CCCCGCGCTCCTCCTCCCTGTAACATGCCATAGTCGCCCTGCGACACACGCGCGGCG 214

Qy 61 GCTAGCGTTGCGCTTCAGCCACCATGGGAATGGGATGGAACAAGATCTGCGCGGCTGT 120

Db 215 GCTAGCGTTGCGCTTCAGCCACCATGGGAATGGGATGGAACAAGATCTGCGCGGCTGT 274

Qy 121 ACATCGCAACTTCAAAAGATGCCAGAGACGGGGAACAATTCAGCAAGAAACAAGGTGACAC 180

Db 275 ACATCGCAACTTCAAAAGATGCCAGAGACGGGGAACAATTCAGCAAGAAACAAGGTGACAC 334

Qy 181 ATATTCTGTCTGCCACGATAGTCCAGGCTATGTTGGAGGGAGTTAAATACCTGTGCA 240

Db 335 ATATTCTGTCTGCCACGATAGTCCAGGCTATGTTGGAGGGAGTTAAATACCTGTGCA 394

Qy 241 TCCAGAGCGGATTCACATCTCAAAACCTGACAAGACATTTCAAGAAAATATTAAT 300

Db 395 TCCAGAGCGGATTCACATCTCAAAACCTGACAAGACATTTCAAGAAAATATTAAT 454

Qy 301 TCATTACAGAGTCCGGCTCGCGGTGAGAGCTCCCTGTACACTGCTGCGCGGGGTCT 360

Db 455 TCATTACAGAGTCCGGCTCGCGGTGAGAGCTCCCTGTACACTGCTGCGCGGGGTCT 514

Qy 361 CCAGAGCGTGACACTGGTGATCGCATACATCATGACCGTCACTGACTTTGGCTGGGAGG 420

Db 515 CCAGAGCGTGACACTGGTGATCGCATACATCATGACCGTCACTGACTTTGGCTGGGAGG 574

Qy 421 ATGCCCTGCACACCGTGGTGCTGGGAGATCCTGTGCCAACCCCAACGTTGGCTTCCAGA 480

Db 575 ATGCCCTGCACACCGTGGTGCTGGGAGATCCTGTGCCAACCCCAACGTTGGCTTCCAGA 634

Qy 481 GACAGCTCCAGGAGTTTGAAGCATGAGGTCATCATGATCGGAGTCCAGTATCGGAGTGAAG 540

Db 635 GACAGCTCCAGGAGTTTGAAGCATGAGGTCATCATGATCGGAGTCCAGTATCGGAGTGAAG 694

Qy 541 AATATGGAGAGAGCCCTTTGAGGATGCAAGAAAGCCCAAAACATTTCTGCCCGCTCCAG 600

Db 695 AATATGGAGAGAGCCCTTTGAGGATGCAAGAAAGCCCAAAACATTTCTGCCCGCTCCAG 754

Qy 601 GAATTCGAAAGTTCTGGGCTTTCTCAGAGACTGTAAATGTACCTGAAGTTTCTGAATA 660

Db 755 GAATTCGAAAGTTCTGGGCTTTCTCAGAGACTGTAAATGTACCTGAAGTTTCTGAATA 814

Qy 661 TTGCARACCCGACAGTTTAGGCTGGTGTGCCAAAAGAAAGCAACATAGTTTAAAG 720

Db 815 TTGCARACCCGACAGTTTAGGCTGGTGTGCCAAAAGAAAGCAACATAGTTTAAAG 874

Qy 721 TATCCAGTAGTGATTTGTAACCTGCTTTTCAATTTGAAGCTGAATATATAGTGTATG 780

Db 875 TATCCAGTAGTGATTTGTAACCTGCTTTTCAATTTGAAGCTGAATATATAGTGTATG 934

Qy 781 TTTATGTTGAGAACTAAGGATATTTTAGCAAGAGAAAATATTTTCCCTTATCCCCAC 840

Db 935 TTTATGTTGAGAACTAAGGATATTTTAGCAAGAGAAAATATTTTCCCTTATCCCCAC 994

Qy 841 TGCTGTGAGGTTTCTGACCTCGCTGGATGCTGTAAAGATCCCGGAGGCTTGGCGC 900

Db 995 TGCTGTGAGGTTTCTGACCTCGCTGGATGCTGTAAAGATCCCGGAGGCTTGGCGC 1054

Qy 901 ACTGCTTTGTGGTGGCTTTGGCGCTC 926



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|||||
1055 ACTGCTTGTGGTGGCTTGGCGCTC 1080

RESULT 14
ABV28356
ID ABV28356 standard; cDNA; 1161 BP.
XX AC
XX ABV28356;
XX DT
XX 16-SEP-2002 (first entry)
XX DE
XX Human prostate expression marker cDNA 28347.
XX KW
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW
XX pharmacogenomic marker; gene; ss.
XX OS
XX Homo sapiens.
XX XX
XX WO200160860-A2.
XX PD
XX 23-AUG-2001.
XX PF
XX 20-FEB-2001; 2001WO-US005171.
XX PP
XX 20-FEB-2001; 2001WO-US005171.
XX PR
XX 17-FEB-2000; 2000US-0183319P.
XX PR
XX 16-MAR-2000; 2000US-0189862P.
XX PR
XX 25-MAY-2000; 2000US-0207454P.
XX PR
XX 09-JUN-2000; 2000US-0211314P.
XX PR
XX 18-JUL-2000; 2000US-0219007P.
XX PR
XX 13-DEC-2000; 2000US-0255281P.
XX PR
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PA
XX Schlegel R, Endege WO, Monahan JE;
XX PI
XX WPI; 2001-662795/76.
XX DR
XX
XX PT
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX PT
XX prostate cells and correlating with presence of prostate cancer, useful
XX PT
XX for detecting presence of prostate cancer, stage of prostate cancer.
XX XX
XX Claim 1; Page 5908-5909; 11750pp; English.
XX XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX CC
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX CC
XX specification or its complement. (I) is useful for: (a) assessing whether
XX CC
XX a patient is afflicted with prostate cancer; (b) monitoring the
XX CC
XX progression of prostate cancer in a patient; (c) assessing the efficacy
XX CC
XX of a test compound to inhibit prostate cancer in a patient; (d) assessing
XX CC
XX the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX CC
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX CC
XX (f) assessing the prostate cell carcinogenic potential of a compound; (g)
XX CC
XX determining whether prostate cancer has metastasized in a patient; (h)
XX CC
XX assessing the aggressiveness or indolence of prostate cancer in a patient
XX CC
XX ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
XX XX
XX Sequence 1161 BP; 301 A; 274 C; 299 G; 278 T; 0 U; 9 Other;
XX SQ

Query Match 96.6%; Score 894.2; DB 5; Length 1161;
Best Local Similarity 99.7%; Pred. No. 3.4e-254;
Matches 896; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 28 GCCATAGTGGCGCTCGGACCAACAGGCGGGCGCTAGCGCTTTCAGCCACCATGG 87
DB 7 GGCCTAGTGGCGCTCGGACCAACAGGCGGGCGCTAGCGCTTTCAGCCACCATGG 66
QY 88 GGAATGGGATGAAAGATGCTGCGCGCGCTGATCGGCAACTTCAAAGATGCCAGAG 147
DB 67 GGAATGGGATGAAAGATGCTGCGCGCGCTGATCGGCAACTTCAAAGATGCCAGAG 126
QY 148 ACGCGGAACAATTGAGCAAGAACAGGTGACACATATTCTGTCTGCCACGATAGTGCA 207
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DB 127 ACGCGGAACAATTGAGCAAGAACAGGTGACACATATTCTGTCTGCCACGATAGTGCCA 186
QY 208 GGCCTATGTTGGAGGGAGTTAAATACTGTGCAATCCAGAGCGGATTCACCATCTCAAA 267
DB 187 GGCCTATGTTGGAGGGAGTTAAATACTGTGCAATCCAGAGCGGATTCACCATCTCAAA 246
QY 268 ACCTGACAAAGACATTTCAAAGAAAGTATTAATTCATTACAGATGCCGCTCCGCGGTG 327
DB 247 ACCTGACAAAGACATTTCAAAGAAAGTATTAATTCATTACAGATGCCGCTCCGCGGTG 306
QY 328 AGAGCTGCCCTTGTACACTGCTGCCGCGGTCTCCAGAGCGTGACACTGGTATCGCAT 387
DB 307 AGAGCTGCCCTTGTACACTGCTGCCGCGGTCTCCAGAGCGTGACACTGGTATCGCAT 366
QY 388 ACATCATGACCGTCACCTGACTTTGGCTGGAGGATGCCCTGCAACACGCTGCTGGGA 447
DB 367 ACATCATGACCGTCACCTGACTTTGGCTGGAGGATGCCCTGCAACACGCTGCTGGGA 426
QY 448 GATCCTGTGCCAACCCCAACGTCGGCTTCCAGAGACAGCTCCAGGAGTTTGAGAGCATG 507
DB 427 GATCCTGTGCCAACCCCAACGTCGGCTTCCAGAGACAGCTCCAGGAGTTTGAGAGCATG 486
QY 508 AGGTCCATCAGTATCGGCAGTGGCTGAAGGAAGATATGAGAGAGAGCCCTTTGACGATG 567
DB 487 AGGTCCATCAGTATCGGCAGTGGCTGAAGGAAGATATGAGAGAGAGCCCTTTGACGATG 546
QY 568 CAGAAGAAAGCAAAACATTTCTGGCGCTCCAGGAATTTCTGAAGTTCTGGGCTTTCTCA 627
DB 547 CAGAAGAAAGCAAAACATTTCTGGCGCTCCAGGAATTTCTGAAGTTCTGGGCTTTCTCA 606
QY 628 GAAGACTGTAATGTACCTGAAGTTTCTGAATATTTGCAAACTTCCAGAGTTTAGGCTGGT 687
DB 607 GAAGACTGTAATGTACCTGAAGTTTCTGAATATTTGCAAACTTCCAGAGTTTAGGCTGGT 666
QY 688 GCTGCCAAAAGAAAGCAACATAGAGTTTAAAGTATCCAGTAGTGAATTTGTAACCTTGT 747
DB 667 GCTGCCAAAAGAAAGCAACATAGAGTTTAAAGTATCCAGTAGTGAATTTGTAACCTTGT 726
QY 748 TTTCATTTGAAGCTGAATATATATACGTAGTCAATGTTTAAAGTATGAGAACTAAGGATATCTT 807
DB 727 TTTCATTTGAAGCTGAATATATATACGTAGTCAATGTTTAAAGTATGAGAACTAAGGATATCTT 786
QY 808 TAGCAGAGAAATATTTTCCCTTATCCCACTGCTGAGAGTTTCTGTACCTCGCTT 867
DB 787 TAGCAGAGAAATATTTTCCCTTATCCCACTGCTGAGAGTTTCTGTACCTCGCTT 846
QY 868 GGATGCTGTAAGGATCCCGGAGCCCTTGGCGCACTGCCCTTGTGGGTGGCTTGGCGCTC 926
DB 847 GGATGCTGTAAGGATCCCGGAGCCCTTGGCGCACTGCCCTTGTGGGTGGCTTGGCGCTC 905

RESULT 15
ABV22541
ID ABV22541 standard; cDNA; 1161 BP.
XX AC
XX ABV22541;
XX DT
XX 13-SEP-2002 (first entry)
XX DE
XX Human prostate expression marker cDNA 22532.
XX KW
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW
XX pharmacogenomic marker; gene; ss.
XX OS
XX Homo sapiens.
XX PN
XX WO200160860-A2.
XX PD
XX 23-AUG-2001.
XX PF
XX 20-FEB-2001; 2001WO-US005171.
XX PR
XX 17-FEB-2000; 2000US-0183319P.
```

PR 16-MAR-2000; 2000US-0189862P.  
PR 25-MAY-2000; 2000US-0207454P.  
PR 09-JUN-2000; 2000US-0211314P.  
PR 18-JUL-2000; 2000US-0219007P.  
PR 13-DEC-2000; 2000US-0255281P.  
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
PA  
XX  
XX Schlegel R, Endege WO, Monahan JE;  
XX  
XX WPI; 2001-662795/76.  
XX  
XX Novel isolated nucleic acid molecule associated with cancerous state of  
PT prostate cells and correlating with presence of prostate cancer, useful  
PT for detecting presence of prostate cancer, stage of prostate cancer.  
XX  
XX Claim 1; Page 3939; 11750pp; English.  
XX  
XX The invention relates to an isolated nucleic acid molecule (I) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
CC specification or its complement. (I) is useful for: (a) assessing whether  
CC a patient is afflicted with prostate cancer; (b) monitoring the  
CC progression of prostate cancer in a patient; (c) assessing the efficacy  
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing  
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)  
CC determining whether prostate cancer has metastasized in a patient; (h)  
CC assessing the aggressiveness or indolence of prostate cancer in a patient  
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker  
XX  
SQ Sequence 1161 BP; 301 A; 274 C; 299 G; 278 T; 0 U; 9 Other;  
  
Query Match 96.6%; Score 894.2; DB 5; Length 1161;  
Best Local Similarity 99.7%; Pred. No. 3.4e-25;  
Matches 896; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 28 GCCATAGTGGCGCTGCGACACACGCGCGGGCGGTAGCGTTGCGCTTCAGCCACCATTGG 87  
DB 7 GGCCTAGTGGCGCTGCGACACACGCGCGGGCGGTAGCGTTGCGCTTCAGCCACCATTGG 66  
  
QY 88 GGAATGGGATGAACAAGATCTGCGCGGGCGGTAGCGTTGCGCTTCAGCCACCATTGG 147  
DB 67 GGAATGGGATGAACAAGATCTGCGCGGGCGGTAGCGTTGCGCTTCAGCCACCATTGG 126  
  
QY 148 ACGGGAACAATTGAGCAAGACAGGTGACACATATCTGCTGTCCACGATAGTGCCA 207  
DB 127 ACGGGAACAATTGAGCAAGACAGGTGACACATATCTGCTGTCCACGATAGTGCCA 186  
  
QY 208 GGCCTATGTTGGAGGAGTTAAATACCTGTGCATCCGAGCGGATTCACCATCTCAA 267  
DB 187 GGCCTATGTTGGAGGAGTTAAATACCTGTGCATCCGAGCGGATTCACCATCTCAA 246  
  
QY 268 ACCTGACAAGACATTTCAAGAAAGATATTAATTCATTACAGAGTCCGGCTCCCGGGTG 327  
DB 247 ACCTGACAAGACATTTCAAGAAAGATATTAATTCATTACAGAGTCCGGCTCCCGGGTG 306  
  
QY 328 AGAGCTGCTTGTACACTGCGCTGGCGGGGTCTCCAGGAGGTTGACACTGGTATCGCAT 387  
DB 307 AGAGCTGCTTGTACACTGCGCTGGCGGGGTCTCCAGGAGGTTGACACTGGTATCGCAT 366  
  
QY 388 ACATCATGACCGCTCACTGACTTTGGCTGGGAGGATGCCCTGCACACCGTGGCTGGGA 447  
DB 367 ACATCATGACCGCTCACTGACTTTGGCTGGGAGGATGCCCTGCACACCGTGGCTGGGA 426  
  
QY 448 GATCTGTGCCAACCCCAACGTTGGGCTTCCAGAGACAGCTCCAGGAGTTGAGAGCATG 507  
DB 427 GATCTGTGCCAACCCCAACGTTGGGCTTCCAGAGACAGCTCCAGGAGTTGAGAGCATG 486  
  
QY 508 AGGTCCATCAGTATCGGCAGTGGCTGAAGGAAGATATGGAGAGAGCCCTTTGCAGGATG 567  
DB 487 AGGTCCATCAGTATCGGCAGTGGCTGAAGGAAGATATGGAGAGAGCCCTTTGCAGGATG 546

QY 568 CAGAAGAGCCAAACAAATTTCTGCGCGCTCCAGGAATTTGAAAGTTTGGGCGCTTTCTCA 627  
DB 547 CAGAAGAGCCAAACAAATTTCTGCGCGCTCCAGGAATTTCTGAAAGTTTGGGCGCTTTCTCA 606  
  
QY 628 GAAGACTGTAAATGTACCTGAAGTTTCTGAATATTTGCAAAACCCGAGAGTTTAGGCTGGT 687  
DB 607 GAAGACTGTAAATGTACCTGAAGTTTCTGAATATTTGCAAAACCCGAGAGTTTAGGCTGGT 666  
  
QY 688 GCTGCCAAAGAAAGCAACATAGAGTTTAAAGTATCCAGTAGTGATTTGTAAACCTTCTT 747  
DB 667 GCTGCCAAAGAAAGCAACATAGAGTTTAAAGTATCCAGTAGTGATTTGTAAACCTTCTT 726  
  
QY 748 TTTCAATTTGAAGCTGAATATATACGTAGTCAATGTTTATGTTGAGAACTTAAGGATATCTT 807  
DB 727 TTTCAATTTGAAGCTGAATATATACGTAGTCAATGTTTATGTTGAGAACTTAAGGATATCTT 786  
  
QY 808 TAGCAAGAGAAATATTTTCCCTTATCCCACTGCTGTGAGAGTTTCTGTACCTCGCTT 867  
DB 787 TAGCAAGAGAAATATTTTCCCTTATCCCACTGCTGTGAGAGTTTCTGTACCTCGCTT 846  
  
QY 868 GGATGCTGTAAAGGATCCCGGAGGCTTGGCGCACTGCTTGTGGGTGGCTTGGCGCTC 926  
DB 847 GGATGCTGTAAAGGATCCCGGAGGCTTGGCGCACTGCTTGTGGGTGGCTTGGCGCTC 905

Search completed: July 21, 2005, 13:31:59  
Job time : 619 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 21, 2005, 17:59:27 ; Search time 334 Seconds  
(without alignments)

282.104 Million cell updates/sec

Title: US-10-658-661-2

Perfect score: 975

Sequence: 1 MGNGWKILPGLYIGNFKDA.....AKNIIAAPGLKFWAFLLRL 184

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	975	100.0	184	2 Q9NRW4	Q9nrw4 homo sapien
2	932	95.6	184	2 Q99N11	Q99n11 mus musculus
3	715	73.3	209	2 Q6GQJ8	Q6gqj8 xenopus lae
4	557	57.1	208	2 Q6DQ06	Q6dgq6 brachydanio
5	544	55.8	209	2 Q6GQ25	Q6gqz9 xenopus lae
6	528	54.2	235	2 Q6PGN7	Q6pgn7 homo sapien
7	482	49.4	327	2 Q8IQK1	Q8iqk1 drosophila
8	482	49.4	447	2 Q9VU80	Q9vu80 drosophila
9	453	46.5	327	2 Q8IQK0	Q8iqk0 drosophila
10	444	45.5	295	1 DUSF_HUMAN	Q9h1r2 homo sapien
11	438	44.9	81	2 Q96AR1	Q96arl homo sapien
12	428	43.9	191	2 Q7PV27	Q7pv27 anopheles g
13	420	43.1	125	1 DUSF_MOUSE	Q84v42 mus musculus
14	297	30.5	201	2 Q86F24	Q86ft24 schistosoma
15	259	26.6	476	2 Q86J73	Q86jit3 dictyosteli
16	257.5	26.4	542	2 Q7PV94	Q7pv94 anopheles g
17	250.5	25.7	483	1 DUSA_MOUSE	Q6es80 mus musculus
18	249.5	25.6	384	2 Q6P9C2	Q6p9c2 homo sapien
19	247.5	25.4	383	2 Q8UW48	Q8uw48 figu rubrip
20	247	25.3	707	2 Q7QTA9	Q7qta9 giardia lam
21	246.5	25.3	177	2 Q8CSL5	Q8cs15 mus musculus
22	246.5	25.3	362	2 Q803B2	Q803b2 brachydanio
23	246.5	25.3	364	2 Q6NYH0	Q6nyh0 brachydanio
24	246.5	25.3	482	1 DUSA_HUMAN	Q6nyw6 homo sapien
25	246.5	25.3	483	2 Q8R3L3	Q8r3l3 m dusp10 pr
26	245.5	25.2	269	2 Q7POA9	Q7pqa9 anopheles g
27	245.5	25.2	354	2 Q8N4A4	Q8n4a4 homo sapien
28	244.5	25.1	384	1 DUS9_HUMAN	Q99956 homo sapien
29	244.5	25.1	378	2 Q91663	Q91663 xenopus lae
30	244.5	25.1	381	1 DUS6_HUMAN	Q16828 homo sapien
31	244.5	25.1	381	1 DUS6_MOUSE	Q9dbb1 mus musculus

32 244.5 25.1 381 1 DUS6\_RAT  
33 244.5 25.1 382 2 Q7T2L9  
34 244.5 25.1 482 2 Q6IAR2  
35 243.5 25.0 476 2 Q3VHV8  
36 243 24.9 653 2 Q7T2T3  
37 243 24.9 691 2 Q6IVY4  
38 243 24.9 694 2 Q68ET3  
39 242.5 24.9 196 2 Q8LPY0  
40 242.5 24.9 198 2 Q9LUG6  
41 242.5 24.9 198 2 Q9R37  
42 242.5 24.9 382 2 Q7T2L8  
43 240.5 24.7 167 2 Q9M8K7  
44 240 24.6 241 2 Q9VW44  
45 240 24.6 290 2 Q86P14

#### ALIGNMENTS

#### RESULT 1

Q9NRW4 ID Q9NRW4 PRELIMINARY; PRT; 184 AA.  
AC Q9NRW4;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Mitogen-activated protein kinase phosphatase x (JNK-stimulating phosphatase 1) (Dual specificity phosphatase 22) (LMW-DSP2).  
GN Name=MKPX; Synonyms=DUSP22, JSP1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Gu J., Huang Q., Yu Y., Xu S., Wang Y., Han Z., Chen Z., Zhou J., Tu Y., Gu W., Fu G., Huang C.;  
RA Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21574601; PubMed=11717427; DOI=10.1073/pnas.231499098;  
RA Shen Y., Luche R., Wei B., Gordon M.L., Diltz C.D., Tonks N.K.;  
RT "Activation of the Jnk signaling pathway by a dual-specificity phosphatase, JSP-1,"  
Proc. Natl. Acad. Sci. U.S.A. 98:13613-13618(2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences,"  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Lung;  
RA Strausberg R.;

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RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RA SEQUENCE FROM N.A.
RA Mao Y., Xie Y., Cheng H.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF165519; AAF66649.1; -
DR EMBL; AF424702; AAL18850.1; -
DR EMBL; BC022847; AAH22847.1; -
DR EMBL; AY249859; AAP76376.1; -
DR HSP; Q16828; IMKP.
DR Genew; HGNC:16077; DUSP22.
DR GO; GO:0006915; P:apoptosis; TAS.
DR GO; GO:0008283; P:cell proliferation; TAS.
DR GO; GO:0007275; P:development; TAS.
DR GO; GO:0000188; P:inactivation of MAPK; TAS.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
DR InterPro; IPR000340; DS_phosphatase.
DR PROSITE; PS000387; TYR_phosphatase.
DR Pfam; PF00782; DSPC; 1.
DR SMART; SM00195; DSPC; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR InterPro; IPR000387; TYR_phosphatase.
DR Pfam; PF00782; DSPC; 1.
DR SMART; SM00195; DSPC; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00054; TYR_PHOSPHATASE_DUAL; 1.
DR KW Kinase.
SQ SEQUENCE 184 AA; 20910 MW; B3F962A087C2BA20 CRC64;

Query Match 100.0%; Score 975; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 5.6e-87;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNGMKNKILPGLYIGNFKDARDAEQLSKNKVTHLSVHDSARPMLEGVKYLICIPAADSPS 60
Db 1 MNGMKNKILPGLYIGNFKDARDAEQLSKNKVTHLSVHDSARPMLEGVKYLICIPAADSPS 60

Qy 61 QNLTRHFKESIKFHECRLRGESCLVHCLAGVSRSVTLVIAYIMTVDFGWEDALHTVRA 120
Db 61 QNLTRHFKESIKFHECRLRGESCLVHCLAGVSRSVTLVIAYIMTVDFGWEDALHTVRA 120

Qy 121 GRSCANPNVGFQRLQEFKEHVEHQYRWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180
Db 121 GRSCANPNVGFQRLQEFKEHVEHQYRWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180

Qy 181 LRRL 184
Db 181 LRRL 184

RESULT 2
Q99N11 PRELIMINARY; PRT; 184 AA.
AC Q99N11;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Dual specificity phosphatase TS-DSP2.
GN Name=Dusp22;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21347909; PubMed=11346645; DOI=10.1074/jbc.M100408200;
RA Aoyama K., Nagata M., Oshima K., Matsuda T., Aoki N.;
RT "Molecular cloning and characterization of a novel dual specificity
RT phosphatase, LMW-DSP2, that lacks the cdc25 homology domain.";
J. Biol. Chem. 276:27575-27583(2001).
DR EMBL; AF237619; AAK15038.1; -
DR HSP; Q16828; IMKP.
DR MGD; MGI:1915926; Dusp22.
DR GO; GO:0005515; P:protein binding; IDA.
DR GO; GO:0046330; P:positive regulation of JNK cascade; IDA.
DR GO; GO:0042127; P:regulation of cell proliferation; IMP.
DR GO; GO:0007179; P:transforming growth factor beta receptor si. .; IMP.

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DR InterPro; IPR000340; DS_phosphatase.
DR InterPro; IPR000387; TYR_phosphatase.
DR Pfam; PF00782; DSPC; 1.
DR SMART; SM00195; DSPC; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00054; TYR_PHOSPHATASE_DUAL; 1.
SQ SEQUENCE 184 AA; 20997 MW; 649553325E88AB577 CRC64;

Query Match 95.6%; Score 932; DB 2; Length 184;
Best Local Similarity 93.5%; Pred. No. 8.9e-83;
Matches 172; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNGMKNKILPGLYIGNFKDARDAEQLSKNKVTHLSVHDSARPMLEGVKYLICIPAADSPS 60
Db 1 MNGMKNKILPGLYIGNFKDARDAEQLSKNKVTHLSVHDSARPMLEGVKYLICIPAADSPS 60

Qy 61 QNLTRHFKESIKFHECRLRGESCLVHCLAGVSRSVTLVIAYIMTVDFGWEDALHTVRA 120
Db 61 QNLTRHFKESIKFHECRLRGESCLVHCLAGVSRSVTLVIAYIMTVDFGWEDALHTVRA 120

Qy 121 GRSCANPNVGFQRLQEFKEHVEHQYRWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180
Db 121 GRSCANPNVGFQRLQEFKEHVEHQYRWLKEEYGENPLRDAEAKNLAAPGILKFWAF 180

Qy 181 LRRL 184
Db 181 LRRL 184

RESULT 3
Q6GQJ8 PRELIMINARY; PRT; 209 AA.
AC Q6GQJ8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE MGC79099 protein.
GN Name=MGC79099;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalek U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;

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"Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative."  
Dev. Dyn. 225:384-391(2002).  
[3]

RP SEQUENCE FROM N.A.  
RC TISSUE=Ovary;  
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC072744; AAH72744.1; -.  
DR GO; GO:0008138; P:protein tyrosine/threonine phosphata. . .; IEA.  
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR000340; DS phosphatase.  
DR InterPro; IPR000387; TYR\_phosphatase.  
DR Pfam; PF00782; DSPC; 1.  
DR SMART; SM00195; DSPC; 1.  
DR PROSITE; PS50056; TYR\_PHOSPHATASE 1; 1.  
DR PROSITE; PS50054; TYR\_PHOSPHATASE\_DUAL; 1.  
SQ SEQUENCE 209 AA; 23485 MW; E83FB752048C902E CRC64;

Query Match 73.3%; Score 715; DB 2; Length 209;  
Best Local Similarity 75.1%; Pred. No. 1.6e-61;  
Matches 127; Conservative 21; Mismatches 21; Indels 0; Gaps 0;  
  
QY 1 MNGGNKILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLGVKYLICIPADSPS 60  
DB 1 MNGGNKILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLGVKYLICIPADSPS 60  
  
QY 61 QNLTRHFKESIKFHEICRLGESCLVHCLAGVSRVTLVIAYIMVTDFGHEDALHTVRA 120  
DB 61 QNLTRHFKESIKFHEICRLGESCLVHCLAGVSRVTLVIAYIMVTDFGHEDALHTVRA 120  
  
QY 121 GRSCANPNVGFQRLQEFKEHVEHVOYRWLKEEYGESPLQDAEAKNLL 169  
DB 121 ARTCANPNMGKQKLEDFGKCEVHFRTWLKDYTESFTHDXDAKQLL 169

RESULT 4  
Q6DQ6 PRELIMINARY; PRT; 208 AA.  
AC Q6DQ6;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Zgc:92816.  
GN Name=zgc:92816;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Strausberg R.;  
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC076284; AAH76284.1; -.  
DR GO; GO:0008138; P:protein tyrosine/threonine phosphata. . .; IEA.  
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR000340; DS phosphatase.  
DR InterPro; IPR000387; TYR\_phosphatase.  
DR Pfam; PF00782; DSPC; 1.  
DR SMART; SM00195; DSPC; 1.  
DR PROSITE; PS00383; TYR\_PHOSPHATASE 1; 1.  
DR PROSITE; PS50056; TYR\_PHOSPHATASE 2; 1.  
DR PROSITE; PS50054; TYR\_PHOSPHATASE\_DUAL; 1.  
KW Hydrolase.  
SQ SEQUENCE 208 AA; 23396 MW; 5B149AE083808854 CRC64;  
  
Query Match 57.1%; Score 557; DB 2; Length 208;  
Best Local Similarity 57.6%; Pred. No. 4.2e-46;  
Matches 98; Conservative 36; Mismatches 36; Indels 0; Gaps 0;  
  
QY 1 MNGGNKILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLGVKYLICIPADSPS 60  
DB 1 MNGGNKILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLGVKYLICIPADSPS 60  
  
QY 61 QNLTRHFKESIKFHEICRLGESCLVHCLAGVSRVTLVIAYIMVTDFGHEDALHTVRA 120  
DB 61 QNLTRHFKESIKFHEICRLGESCLVHCLAGVSRVTLVIAYIMVTDFGHEDALHTVRA 120  
  
QY 121 GRSCANPNVGFQRLQEFKEHVEHVOYRWLKEEYGESPLQDAEAKNLL 170  
DB 121 VRSFVGNPGYQQLQEFQKQVSEYQAWLRASRSPFFKQEQVEALLS 170

RESULT 5  
Q6GQZ9 PRELIMINARY; PRT; 209 AA.  
AC Q6GQZ9;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE MGC82394 protein.  
GN Name=MGC82394;  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Heart;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";

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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Klein S., Gerhard D.S.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC071144; AAH71144.1; -
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0008138; F:protein tyrosine/serine/threonine phosphata. .; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000340; DS_phosphatase.
DR InterPro; IPR000387; TYR_phosphatase.
DR Pfam; PF00782; DSPC; 1.
DR SMART; SM00195; DSPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00054; TYR_PHOSPHATASE_DUAL; 1.
DR Hydrolase.
SQ SEQUENCE 209 AA; 23975 MW; F79333CAAB9459E9B CRC64;

Query Match 55.8%; Score 544; DB 2; Length 209;
Best Local Similarity 55.9%; Pred. No. 7, 9e-45;
Matches 95; Conservative 37; Mismatches 38; Indels 0; Gaps 0;

Qy 1 MNGGNKILPGLYTGNGFKDARDQSLSKNVTHILSVHDSARPMLGVKYLCPAADSPPS 60
Db 1 MGGGSKIVDGLYGNIRDSKATLNRNGITHTIVSVHNAKPVQLQNTYLCISASDSS 60

Qy 61 QNLTTHFKESIKFTHCECLRGESCLVHCLAGVSRTLVIAVIMTVDFGHWEDALHTVRA 120
Db 61 QNLTQHFKQCIKFTHESLHGGGCLVHCLAGVSRTMLVAYLMTVTFNGDECLSAVRS 120

Qy 121 GRSCANPNVGFORQLOEPEKHEVHQYRWLKEEYGESPLQDAEAKNILA 170
Db 121 VRSYVGNFGQQLOEYEMTLVKEYRWLQEGVGRPFNDQDKVQLLIA 170

Qy 121 GRSCANPNVGFORQLOEPEKHEVHQYRWLKEEYGESPLQDAEAKNILA 170
Db 121 VRSYVGNFGQQLOEYEMTLVKEYRWLQEGVGRPFNDQDKVQLLIA 170

Qy 121 GRSCANPNVGFORQLOEPEKHEVHQYRWLKEEYGESPLQDAEAKNILA 169
Db 121 TRTPANPNPGRQLEEFEGWASSQKLARQLERGESPFDESELRAILL 169

Qy 121 GRSCANPNVGFORQLOEPEKHEVHQYRWLKEEYGESPLQDAEAKNILA 169
Db 121 TRTPANPNPGRQLEEFEGWASSQKLARQLERGESPFDESELRAILL 169

RESULT 6
Q6PGN7 PRELIMINARY; PRT; 235 AA.
AC Q6PGN7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Dual specificity phosphatase-like 15, isoform a.
GN Name=DUSP15;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K.J., Evans G., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merklov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weisenbach J.,  
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
RA Yen R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*.";  
RL Science 287:2185-2195 (2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426065; PubMed=12537568;  
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,  
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*  
RT *melanogaster* euchromatic genome sequence.";  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426070; PubMed=12537573;  
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celniker S.E.;  
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
RT a genomics perspective.";  
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426069; PubMed=12537572;  
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
RT systematic review.";  
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).  
RN [5]  
RP SEQUENCE FROM N.A.  
RX FlyBase;  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RX FlyBase;  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A.  
RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,

RA Park S., Wan K., Yu C., Rubin G.M., Celniker S.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
RA EMBL; AE003537; AAN11825.1; -;  
DR EMBL; BT014928; AAT47779.1; -;  
DR HSSP; Q16828; IMKP  
DR FlyBase; FBgn0036369; CG10089.  
DR GO; GO:0008138; P:protein tyrosine/serine/threonine phosphorylation; IEA.  
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR000340; DS phosphatase.  
DR InterPro; IPR000387; TVR\_phosphatase.  
DR Pfam; PF00782; DSPC; 1.  
DR SMART; SM00195; DSPC; 1.  
DR PROSITE; PS00056; TYR\_PHOSPHATASE 2; 1.  
DR PROSITE; PS0054; TYR\_PHOSPHATASE DUAL; 1.  
SQ SEQUENCE 327 AA; 36855 MW; 2DAEF208A43FAE3 CRC64;  
  
Query Match 49.4%; Score 482; DB 2; Length 327;  
Best Local Similarity 51.8%; Pred. No. 1.5e-38;  
Matches 86; Conservative 36; Mismatches 44; Indels 0; Gaps 0;  
  
Qy 1 MGNMKNILPGLYTGNFKDARDAEQLSKNKTHTLSVHDSARPMLEGVKYLCPAADSPS 60  
Db 1 MGNMKNVLPGLYGVNVRDSKHAQLERFKLSHIAHDSPRLLPKHYLCVMSDTPD 60  
Qy 61 QNLTRFKESIKFTHECRLEGESCLVHCLAGVSRSVTLVIAYIMTVDFGWEDALHTVRA 120  
Db 61 QNLSQYFSCVNCDFIHAARLRGNVLHCLAGRSRSTVAVAYIMTATHLNKEALKVVRA 120  
Qy 121 GRSCANFNVGFQRLQEFKEHVEHQYRWLKEEYGESPLQDAEAK 166  
Db 121 GRAVNPAGFSQLOEFQFKLSERRRLRERFPSSALEQLDRTK 166  
  
RESULT 8  
Q9VU80 PRELIMINARY; PRT; 447 AA.  
ID Q9VU80  
AC Q9VU80;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE CG10089-PD.  
GN ORFNames=CG10089;  
OS *Drosophila melanogaster* (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_taxid=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,  
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beson K.Y., Bens P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,



RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,  
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstock G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila  
RT melanogaster euchromatic genome sequence."  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426070; PubMed=12537573;  
RA Kaminker J.S., Bergman C.M., Drommler B., Carlson J., Svirkas R.,  
RA Patel S., Frise E., Wheeler K.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celniker S.E.;  
RT "The transposable elements of the Drosophila melanogaster euchromatin:  
RT a genomics perspective."  
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426069; PubMed=12537572;  
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
RT systematic review."  
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).  
RN [5]  
RP SEQUENCE FROM N.A.  
RX Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
RA FlyBase;  
RL Submitter (SEP-2002) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RX Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
RA EMBL; AE001537; AAN11827.1; -  
DR HSSP; Q16828; 1MKP.  
DR FlyBase; FBgn0036369; CG10089.  
DR GO; GO:0008138; P:protein tyrosine/serine/threonine phosphorylation; IEA.  
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.  
DR InterPro; IPR000340; DS phosphatase.  
DR InterPro; IPR000387; TYR\_phosphatase.  
DR Pfam; PF00782; DSPC; 1.  
DR SMART; SM00195; DSPC; 1.  
DR PROSITE; PS00056; TYR\_PHOSPHATASE 2; 1.  
DR PROSITE; PS00054; TYR\_PHOSPHATASE DUAL; 1.  
SQ SEQUENCE 327 AA; 37007 MW; F79A75EC9CAE9BC7 CRC64;  
  
Query Match 46.5%; Score 453; DB 2; Length 327;  
Best Local Similarity 50.0%; Pred. No. 1e-35;  
Matches 81; Conservative 36; Mismatches 45; Indels 0; Gaps 0;  
  
Qy 5 MNKILPGLYIGNFKDARDAEQLSKNVTHLSVHDSAPMLLEGVKYLCIPADSPSONLT 64  
Db 5 MGKVLPLGVNGYRDSKDAQLERFKSHIATIDSPRLPLPKHYLCVWASDTPDQNL 64  
Qy 65 RHFKESTIKFIECHRLGSGCLVHCLAGVSRSVTLLVIAYIMTVTFGWEDALHTVRGSC 124  
Db 65 QYFVSCVNDFIHAARLREGNVLHCLAGVSRSVTVAIVMTATLHNKELKVVVRAGRAV 124  
Qy 125 ANPNVGFQRLQEFKEHVQVROWLKEEYGESPLQDAEAK 166  
Db 125 ANPNAGFQSLQEFQFLSEERRRLRRFRFPSSALEQLDRTK 166  
  
RESULT 10  
ID DUSF HUMAN STANDARD; PRT; 295 AA.  
AC Q9H1R2; Q9N826; Q9BX24;  
DT 28-FEB-2003 (Rel. 41, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DE 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Dual specificity protein phosphatase 15 (EC 3.1.3.48) (EC 3.1.3.16).  
GN Name=DUSP15; Synonyms=C20orf57;  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Testis;  
RX PubMed=14702039; DOI=10.1038/ng1285;  
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,  
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,  
RA Sekine M., Ohayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,  
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,  
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,  
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,  
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,  
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,  
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,  
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y.,  
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Horuta T.,  
RA Kubano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,  
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,  
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,  
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,  
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,  
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,  
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,  
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,  
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,  
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;  
RT "Complete sequencing and characterization of 21,243 full-length human  
RT cDNAs."  
RL Nat. Genet. 36:40-45(2004).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21639749; PubMed=11780052; DOI=10.1038/414865a;  
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,  
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,  
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,  
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
RA Coulson A.G., Coville G.J., Deadman R., Dhami P.D., Dunn M.,  
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.M., Lawlor S.,  
RA Lehar V.L., Martin S.L., Levensha M.A., Lloyd C., Lloyd D.M., Lawlor S.,  
RA Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.A.,  
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,  
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
RA Rogers J.;  
RT "The DNA sequence and comparative analysis of human chromosome 20."  
RL Nature 414:865-871(2001).



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Db 1 MTVTDFGWEDALHTVGRGSCANPNVGFQRLQEFKEHVEHQYRWLKEEYGESPLQDAE 60
QY 164 EAKNIIAAPGILKFWAFRLRL 184
Db 61 EAKNIIAAPGILKFWAFRLRL 81

RESULT 12
Q7PV27 ID Q7PV27 PRELIMINARY; PRT; 191 AA.
AC Q7PV27;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DE ENSANGP0000016462 (Fragment).
GN Name=ENSANGG0000013973;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RL Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AA0501008986; EAA00578.2; -.
DR HSSP; P51452; 1JX4.
DR GO; GO:0008139; P:protein tyrosine/serine/threonine phosphata. .; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000340; DS_phosphatase.
DR InterPro; IPR000387; TYR_phosphatase.
DR Pfam; PF00782; DSPC; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00054; TYR_PHOSPHATASE_DUAL; 1.
FT NON_TER 1
FT NON_TER 191
SQ SEQUENCE 191 AA; 21875 MW; 28DA4C22B83B853D CRC64;

Query Match 43.9%; Score 428; DB 2; Length 191;
Best Local Similarity 48.8%; Pred. No. 1.5e-33;
Matches 80; Conservative 36; Mismatches 48; Indels 0; Gaps 0;

QY 7 KILPGLYGNFKDARDAEQLSKNKKVTHLSVHDSARPMLEGVKYLICIPAADSPQNLTNRH 66
Db 1 QVMPGLYIGNYRDSKYQQLDRYGITHIVSIHDSPRFHPDKHYLCVIAADKPDQNLQY 60
QY 67 FKESIKFTHECRLGESCLVHCLAGVSRVTLVIAYIMTVTDFGWEDALHTVGRGSCAN 126
Db 61 FSVCNDFHSLARKQGVNLHCLAGMSRVTVAVAYIMCVTPLSKWELKVVGRGSIAN 120
QY 127 PNVGQRQLQEFKEHVEHQYRWLKEEYGESPLQDAEAKNIIA 170
Db 121 PNLGPNQLQDFETNKLTEERRRLKRPFSLALELTDEKQCYLE 164

RESULT 13
DUSF_MOUSE ID DUSF_MOUSE STANDARD; PRT; 125 AA.
AC Q8RAV2;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE Dual specificity protein phosphatase 15 (EC 3.1.3.48) (Fragment).
DE (Dual specificity protein phosphatase T-DSP10) (Fragment).
GN Name=Dusp15;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
```

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RP SEQUENCE FROM N.A. (ISOFORM 2), AND TISSUE SPECIFICITY.
RX MEDLINE=21326039; PubMed=11432789;
RA Aoki N., Aoyama K., Nagata M., Matsuda T.;
RT "A growing family of dual specificity phosphatases with low molecular
RT masses.";
RL J. Biochem. 130:133-140(2001).
[2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=21671825; PubMed=11812828; DOI=10.1093/nar/29.24.4983;
RA Mu X., Zhao S., Pershad R., Haiech T.-F., Scarpa A., Wang S.W.,
RA White R.A., Beremand P.D., Thomas T.L., Gan L., Klein W.H.;
RT "Gene expression in the developing mouse retina by EST sequencing and
RT microarray analysis.";
RL Nucleic Acids Res. 29:4983-4993(2001).
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q8RAV2-1; Sequence=Displayed;
CC Note=Derived from EST data;
CC Name=2;
CC IsoId=Q8RAV2-2; Sequence=VSP_007294, VSP_007295;
CC Note=Inactive. Lacks the active site;
CC TISSUE SPECIFICITY: Isoform 2 is highly expressed in testis.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class dual specificity subfamily.
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EMBL; AF357887; AAM00226.1; -
EMBL; BU924460; -; NOT_ANNOTATED_CDS.
HSSP; P51452; 1VHR.
MGD; MGI:1934928; Dusp15.
InterPro; IPR000340; DS_phosphatase.
InterPro; IPR000387; TYR_phosphatase.
Pfam; PF00782; DSPC; 1.
SMART; SM00195; DSPC; 1.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS00054; TYR_PHOSPHATASE_DUAL; 1.
KW Alternative splicing; Hydrolase; Protein phosphatase.
FT DOMAIN 65 -125 Protein-tyrosine phosphatase.
FT ACT_SITE 88 88 Phosphocysteine intermediate (By
similarity).
FT VARSPLIC 88 105 CFAGISRSTTVIAYVMT -> WPLKHECRARSLSLQCS
(in isoform 2).
FT VARSPLIC 106 125 /FTid=VSP_007294.
FT VARSPLIC 125 125 Missing (in isoform 2).
FT NON_TER 125 125 /FTid=VSP_007295.
SQ SEQUENCE 125 AA; 13797 MW; D79F87FF0120F816 CRC64;

Query Match 43.1%; Score 420; DB 1; Length 125;
Best Local Similarity 56.0%; Pred. No. 5.4e-33;
Matches 70; Conservative 26; Mismatches 29; Indels 0; Gaps 0;

QY 1 MGNQMKILPGLYGNFKDARDAEQLSKNKKVTHLSVHDSARPMLEGVKYLICIPAADSPS 60
Db 1 MGNQMKVLPGLYGNFKDARDAEQLSKNKKVTHLSVHDSARPMLEGVKYLICIPAADSPS 60
QY 61 QNLTFRHFKESIKFTHECRLGESCLVHCLAGVSRVTLVIAYIMTVTDFGWEDALHTVRA 120
Db 61 VPIKKHFKECVHFTHSCRLNGNCLVHCFCAGISRSTTVIAYVMTVTGLGHWQEVLEAIKA 120
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Qy 121 GRSCA 125
Db 121 SRPTA 125

RESULT 14
Q86F24 PRELIMINARY; PRT; 201 AA.
ID Q86F24
AC Q86F24;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Clone Z2D1174 mRNA sequence.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2287925; PubMed=12973349; DOI=10.1038/ngl236;
RA Hu W., Yan Q., Shen D.K., Liu F., Zhu Z.D., Song H.D., Xu X.R.,
RA Wang S.J., Rong Y.P., Zeng L.C., Wu J., Zhang X., Wang J.J., Xu X.N.,
RA Wang S.Y., Fu G., Zhang X.L., Wang Z.Q., Brindley P.J., McManus D.P.,
RA xue C.L., Feng Z., Chen Z., Han Z.G.;
RT "Evolutionary and biomedical implications of a Schistosoma japonicum
RT complementary DNA resource.";
RL Nat. Genet. 35:139-147(2003).
DR EMBL; AY223040; AAP06063.1; -.
DR HSSP; Q16828; 1MKP.
DR GO; GO:0008138; P:protein tyrosine/serine/threonine phosphata. .; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000340; DS_phosphatase.
DR InterPro; IPR000387; TYR_phosphatase.
DR Pfam; PF00782; DSPC; 1.
DR SMART; SM00195; DSPC; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
SQ SEQUENCE 201 AA; 22013 MW; F43ACCSA4C1D85B7 CRC64;

Query Match 30.5%; Score 297; DB 2; Length 201;
Best Local Similarity 40.8%; Pred. No. 9.8e-21;
Matches 69; Conservative 28; Mismatches 66; Indels 6; Gaps 4;

Qy 1 MGNMKNILPGLYGNFKDARDAEQLSKNKNVTHLSVHDSARPMLGKVKYLCIPADSP 59
Db 1 MGSMSKIVPLGYGVGASQSLDENGITHVCVSLHYNFK-CPSRKQIILRADDD 58
Qy 60 SONLTHRFKESIKTFHECRLGESCLVHCAGVSRVTLVIAYIMTVDFGWEDALHTVR 119
Db 59 KENTAKYFRDACFFIHEARVYNGAVLHCACGVSRVTLVIAYIMTVTNMPLKLVRAV 118
Qy 120 AGRSCANPNVGFQLOFEKX-EVHQYRWLKEEYGESPLQ--DABEA 165
Db 119 GARPCCAFNSGFLEQIEFGKSGAAAKVQELIAYVGEWPKEKLDADIA 167

RESULT 15
Q86J73 PRELIMINARY; PRT; 476 AA.
ID Q86J73
AC Q86J73;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Similar to dual-specificity protein phosphatase; protein id:
DE At3g23610.1.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=AX4;
RC MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
RX Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,

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RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tungal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RL Nature 418:79-85(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RC Baumgart C.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC116984; AAO51441.1; -.
DR HSSP; Q16828; 1MKP.
DR GO; GO:0008138; P:protein tyrosine/serine/threonine phosphata. .; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000340; DS_phosphatase.
DR InterPro; IPR001763; Rhodanese-like.
DR InterPro; IPR000387; TYR_phosphatase.
DR Pfam; PF00782; DSPC; 1.
DR SMART; SM00195; DSPC; 1.
DR SMART; SM00450; RHOD; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; UNKNOWN_1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50054; TYR_PHOSPHATASE_DUAL; 1.
SQ SEQUENCE 476 AA; 53798 MW; FF4F47417971D26F CRC64;

Query Match 26.6%; Score 259; DB 2; Length 476;
Best Local Similarity 34.2%; Pred. No. 1.4e-16;
Matches 55; Conservative 35; Mismatches 57; Indels 14; Gaps 4;

Qy 2 GNGMKNILPG-----LYIGNFKDARDAEQLSKNKNVTHLSVH---DSARPMLGKVKYL 52
Db 201 GGGGSQLYPSFIIKDFLYLGAENAGNRQQLINKITHLVNMAGELDDVYPHL--YKYR 258
Qy 53 IPAADSPSONLTHRFKESIKTFHECRLGESCLVHCAGVSRVTLVIAYIMTVDFGWE 112
Db 259 ANLDDREKANIYEHFEPVIQFINCKKQGRVLHCAMGISRSSTVVLAYLMKEDHMTYS 318
Qy 113 DALHTVRAGRSCANPNVGFQLOFEKXPEKHEVHQYRWLKEE 153
Db 319 DAFTFCQKRSCLNPNFGVKQLKDYQOHLT---LEWEKQE 356

Search completed: July 21, 2005, 19:02:21
Job time : 336 secs

```



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 21, 2005, 18:05:42 ; Search time 65 Seconds  
(without alignments)  
272.367 Million cell updates/sec

Title: US-10-658-661-2

Perfect score: 975

Sequence: 1 MGNMKNILPGLYIGNFKDA.....AKNLAAPGILKFWAFLLRL 184

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_79.\*

1: PIR1.\*

2: PIR2.\*

3: PIR3.\*

4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	240	24.6	619	2 T15969	hypothetical prote
2	238.5	24.5	365	2 T32494	hypothetical prote
3	237.5	24.4	330	2 T39698	protein tyrosine p
4	234	24.0	223	2 T49365	protein tyrosine p
5	229.5	23.5	276	2 T48906	protein tyrosine p
6	224	23.0	205	2 T49364	protein tyrosine p
7	221.5	22.7	384	1 T38890	dual specificity p
8	218	22.4	866	2 F88481	protein C16A3.1 [1
9	210.5	21.6	220	2 JC7885	low-molecular-mass
10	203.5	20.9	303	2 T46405	hypothetical prote
11	203.5	20.9	393	2 A56947	dual specificity p
12	201.5	20.7	142	2 T03074	dual specificity p
13	201.5	20.7	394	2 A56115	dual specificity p
14	195.5	20.1	314	1 A57126	dual specificity p
15	194.5	19.9	367	1 S29030	dual specificity p
16	190.5	19.5	186	2 T16056	hypothetical prote
17	190.5	19.5	314	2 B57126	dual specificity p
18	189	19.4	185	1 A47196	dual specificity p
19	185.5	19.0	367	1 S24411	dual specificity p
20	185.5	19.0	367	2 S2265	dual specificity p
21	184.5	18.9	364	1 S31304	protein-tyrosine-p
22	176	18.1	226	2 T21380	hypothetical prote
23	175	17.9	272	2 T18915	hypothetical prote
24	169.5	17.4	171	1 QOV2H1	dual specificity p
25	166.5	17.1	171	1 A42514	dual specificity p
26	163.5	16.8	171	1 T36845	dual specificity p
27	163.5	16.8	171	2 T28522	probable dual spec
28	163.5	16.8	171	2 B72161	JIL protein - vari
29	160.5	16.5	171	1 B47452	dual specificity p

30	156.5	16.1	771	2 T47666	phosphatase-like p
31	153	15.7	272	2 T19418	hypothetical prote
32	136	13.9	283	2 G84458	probable protein p
33	135.5	13.9	600	2 T18446	hypothetical prote
34	135	13.8	580	2 T18439	hypothetical prote
35	130.5	13.4	292	2 S41012	hypothetical prote
36	125.5	12.9	489	1 S58725	dual specificity p
37	120.5	12.4	209	1 S48459	probable dual spec
38	117	12.0	204	2 T17802	hypothetical prote
39	114	11.7	169	2 T30684	probable dual spec
40	113	11.6	150	2 T21489	hypothetical prote
41	101.5	10.4	807	1 S44538	probable protein-t
42	100.5	10.3	278	2 T39517	dual-specificity M
43	100.5	10.3	597	1 S43743	probable dual spec
44	98.5	10.1	430	2 E90880	probable enzymes I
45	98.5	10.1	430	2 D85738	probable enzymes Y

ALIGNMENTS

RESULT 1

T15969

hypothetical protein F08B1.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004

C:Accession: T15969

R:Chisose, S.

submitted to the EMBL Data Library, July 1995

A:Description: The sequence of C. elegans cosmid F08B1.

A:Reference number: Z18439

A:Accession: T15969

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-619 <CHI>

A:Cross-references: UNIPROT:Q10038; EMBL:U23178; NID:G726421; PID:G726422; PIDN:AAC46719.

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:F08B1.1

A:Introns: 22/2; 57/1; 99/1; 160/3; 252/2; 549/3

Query Match 24.6%; Score 240; DB 2; Length 619;  
Best Local Similarity 32.9%; Pred. No. 7.2e-15;  
Matches 56; Conservative 33; Mismatches 69; Indels 12; Gaps 3;

Qy	2	GNGMKNILPGLYIGNFKDAEQLSKNKVTHLSVHDSARPML---EGVKYLCPAADS	58
Db	135	GDGITLTPNIYLGSDLSLDTMLDALDISVWNLSTCPKSCVCIKEDKNFMRIPVNDS	194
Qy	59	PSQNLTRHFKESIKFIHECLRGSSCLVHCLAGVSRVTLVIAYIMTVDGWDALHTV	118
Db	195	YQEKLSYFPWFVBLEKCRAGKKKLIHCLAGISRSPTLAISYIMRYMKMGSDDAYRYV	254
Qy	119	RAGRSANPNVGFQRLQEFEE---KHEVHQYRWLK-----EYGESPL	159
Db	255	KEREPSISPNFNGQLLEVENVLKHVLDYNAQSRPHRMVDYGFSDL	304

RESULT 2

T32494

hypothetical protein C05B10.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004

C:Accession: T32494

R:Geisel, C.; Wamsley, P.

submitted to the EMBL Data Library, December 1997

A:Description: The sequence of C. elegans cosmid C05B10.

A:Reference number: Z21178

A:Accession: T32494

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-365 <GBI>

A:Cross-references: UNIPROT:O44128; EMBL:AF036685; PIDN:AAB88308.1; GSPDB:GN00022; CESP:



A:Experimental source: strain Bristol N2; clone C05B10  
C:Genetics:  
A:Gene: CESP:C05B10.1  
A:Map position: 4  
A:Introns: 22/2; 46/2; 74/3; 163/2; 204/2; 248/1; 287/2

Query Match 24.5%; Score 238.5; DB 2; Length 365;  
Best Local Similarity 37.2%; Pred. No. 5.3e-15;  
Matches 51; Conservative 28; Mismatches 55; Indels 3; Gaps 1;

Qy 7 KILPGLYIGNFKDARDAEQLSKNKVTILSVHDSARPMLE---GVKYLCPAADSPOQL 63  
Db 183 KLTNFLVIGNAETAKNRDLVKKYSISHVINVTSLNPTFEEDPNRYLRISADDNASHNL 242

Qy 64 TRHPKESIKFIHECRLRGESCLVHCLAGVRSVTLVIAYIMTVDFGWEDALHTVRA 123  
Db 243 TKFPPEAISFIDARRNDSACLHCLAGISRSVTICLAYLMKTEMCTLDSAYEVQKRNA 302

Qy 124 CANPNVGFQRLQEFK 140  
Db 303 SIAPNFHFMGLTDYEK 319

RESULT 3  
T39698  
protein tyrosine phosphatase - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: T39698  
R:Wood, V.; Skelton, J.; Churcher, C.M.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, July 1999  
A:Reference number: Z21870  
A:Accession: T39698  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-330 <WOO>  
A:Cross-references: UNIPROT:O13632; EMBL:AL109652; PIDN:CAB51765.1; GSPDB:GN00067  
A:Experimental source: strain 972h; cosmid c17A3  
C:Genetics:  
A:Gene: p1041  
A:Map position: 2

Query Match 24.4%; Score 237.5; DB 2; Length 330;  
Best Local Similarity 35.8%; Pred. No. 5.8e-15;  
Matches 58; Conservative 29; Mismatches 66; Indels 9; Gaps 3;

Qy 3 NGMKNILPGLYIGNFKDARDAEQLSKNKVTILSVHDSARPMLE--GVKYLCPAADS 60  
Db 45 NDLSEISKVLYISSMKTASELVSTSDKGIDYTLSAM-SINPNLSVPBQOHLWLQIEDSS 103

Qy 61 QNLTRHPKESIKFIHECRLRGESCLVHCLAGVRSVTLVIAYIMTVDFGWEDALHTVRA 120  
Db 104 QNLLQYFEKSNKFTAFALSKNAKVLVHCFAGISRSVTLVAAYLMKENNWNTEALSHINE 163

Qy 121 GRSCANPNVGFQRLQEFK-----HEVHYRWMLKEEYCE 156  
Db 164 RRGISPNANFLQRLVYFCNYQLDRSLRPYRWLFRYGD 205

RESULT 4  
I49365  
protein tyrosine phosphatase - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I49365  
R:Wishart, M.J.; Denu, J.M.; Williams, J.A.; Dixon, J.E.  
J. Biol. Chem. 270, 26782-26785, 1995  
A:Title: A single mutation converts a novel-phosphotyrosine binding domain into a dual-s  
A:Reference number: I49364; MUID:96070766; PMID:7592916  
A:Accession: I49365  
A:Status: preliminary;  
A:Molecule type: mRNA  
A:Residues: 1-223 <RES>

A:Cross-references: UNIPROT:Q60969; EMBL:U34973; NID:gl063624; PIDN:AAA87037.1; PID:gl063  
C:Genetics:  
A:Introns: 168/3  
F:36-174/Domain: VHL-type dual specificity phosphoprotein phosphatase homology <VHL>

Query Match 24.0%; Score 234; DB 2; Length 223;  
Best Local Similarity 36.7%; Pred. No. 7.8e-15;  
Matches 54; Conservative 26; Mismatches 59; Indels 8; Gaps 3;

Qy 1 MGNMKNILPGLYIGNFKDARDAEQ--LSKNKVTILSVHDS-----ARPMLEGV-KYLC 52  
Db 25 MRREMQLVGLFLGPPVSSAMSKSLPILOKHGITHIICIRQNIETANFIKENFQQLPRYLV 84

Qy 53 IPAADSPQNLTRHPKESIKFIHECRLRGESCLVHCLAGVRSVTLVIAYIMTVDFGWE 112  
Db 85 LDIAADPNVENIIRFFPMTKFIDGSLQNGKVLVHGNAGISRSAAAFVIAYIMETFGMKYR 144

Qy 113 DALHTVRAGRSCANPNVGFQRLQEFK 139  
Db 145 DAFAYQERRFCINPNAGFVHQLQEYE 171

RESULT 5  
T48906  
protein-tyrosine-phosphatase [EC 3.1.1.3.48] [imported] - Chlamydomonas eugametos  
C:Species: Chlamydomonas eugametos  
C:Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 09-Jul-2004  
C:Accession: T48906  
R:Haring, M.A.; Siderius, M.; Joank, C.; Hirt, H.; Walton, K.M.; Musgrave, A.  
Plant J. 7, 981-988, 1995  
A:Title: Tyrosine phosphatase signalling in a lower plant: cell-cycle and oxidative stres  
A:Reference number: Z25005; MUID:95323001; PMID:7599654  
A:Accession: T48906  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-276 <HAR>  
A:Cross-references: UNIPROT:Q39491; EMBL:X77938; NID:g992593; PIDN:CAA54910.1; PID:g9925  
A:Experimental source: strain UTEX 10  
C:Genetics:  
A:Gene: VH-PTP13  
C:Keywords: phosphoric monoester hydrolase

Query Match 23.5%; Score 229.5; DB 2; Length 276;  
Best Local Similarity 35.9%; Pred. No. 2.7e-14;  
Matches 55; Conservative 25; Mismatches 66; Indels 7; Gaps 3;

Qy 8 ILPG-LYIGNFKDARDAEQLSKNKVTILSVHDSARPMLEG-VKYLCPAADSPOQLTR 65  
Db 90 IVPGLILSSCEVESESELTLKLGVTILQVGEELKPSHPGRFTYLSLPILDMEGQDIVA 149

Qy 66 HFKESIKFIHECRLRGESCLVHCLAGVRSVTLVIAYIMTVDFGWEDALHTVRAGRSCA 125  
Db 150 LLPSCFQLQQAQASGGVCLVHCLAGISRSASVVVIAIYMTQGMPTTEARAVRRARSKV 209

Qy 126 NPNVGFQRLQEFKHEVHYRWMLKEEYCESP 158  
Db 210 YPMTGFTLQLQELDRLRRESGAIQW-----GDTTP 237

RESULT 6  
I49364  
protein tyrosine phosphatase - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 15-Mar-2004  
C:Accession: I49364  
R:Wishart, M.J.; Denu, J.M.; Williams, J.A.; Dixon, J.E.  
J. Biol. Chem. 270, 26782-26785, 1995  
A:Title: A single mutation converts a novel-phosphotyrosine binding domain into a dual-s  
A:Reference number: I49364; MUID:96070766; PMID:7592916  
A:Accession: I49364  
A:Status: preliminary;  
A:Molecule type: mRNA  
A:Residues: 1-205 <RES>

A:Cross-references: EMBL:U34973; NID:gl063624; PIDN:AA87036.1; PID:gl063625  
F:36-174/Domain: Vhl-type dual specificity phosphoprotein phosphatase homology <VH1>

Query Match 23.0%; Score 224; DB 2; Length 205; .  
Best Local Similarity 32.8%; Pred. No. 6.4e-14;  
Matches 57; Conservative 28; Mismatches 67; Indels 22; Gaps 5;

Qy 1 MNGMKILPGLYIGNFKDARDABQ--LSKNKVTHTLSVHDS-----ARPMLEGV-KYLC 52

Db 25 MRREMOEVLPLGLPYSSAMKSLPILOKHGITHICIRQNIENAFIKPNFQQLRYLV 84

Qy 53 IPADSPSONLTRFKESIKFIHECRLRGESCLVHCLAGVSRVTLVIAYITMTDQWE 112

Db 85 LDIADNPVENTIRFPMTKEPIDGSLQNGKGVLVHGNAGISRAAFVIAYIMETFGMKYR 144

Qy 113 DALHTVTRAGSCAMPNVGFQRLQEFKEHVEHYQVWMLKEVYGES---PLQDAE 163

Db 145 DAFYVQRRFCINPAGF-----VHQLQMLSWNSARSAPLPKQK 187

## RESULT 7

I38890 dual specificity phosphoprotein phosphatase (EC 3.1.1.3 -) 5 - human

N:Alternate names: dual specificity phosphatase B23; dual-specificity phosphatase hvh-3;

C:Species: Homo sapiens (man)

C:Date: 16-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004

C:Accession: I38890; A55313

R:Kwak, S.P.; Dixon, J.E.

J. Biol. Chem. 270, 1156-1160, 1995

A:Title: Multiple dual specificity protein tyrosine phosphatases are expressed and regul

A:Reference number: A55432; MUID:95138103; PMID:7836374

A:Accession: I38890

A:Molecule type: mRNA

A:Residues: 1-384 <RES>

A:Cross-references: UNIPROT:Q16690; EMBL:U16996; NID:9642012; PIDN:AA806261.1; PID:96420

A:Experimental source: placenta

R:Ishibashi, T.; Bottaro, D.P.; Michieli, P.; Kelley, C.A.; Aaronson, S.A.

J. Biol. Chem. 269, 29897-29902, 1994

A:Title: A novel dual specificity phosphatase induced by serum stimulation and heat shock

A:Reference number: A55313; MUID:95050849; PMID:7961985

A:Accession: A55313

A:Molecule type: mRNA

A:Residues: 1-6, 'GHV', 12-70, 'R', 72-104, 'P', 107-362, 'RCILPTQSSSAAELWQRNPARTGMEEAQQOEQI

A:Cross-references: GB:U15932; NID:9606971; PIDN:AAA64693.1; PID:9606972

A:Experimental source: mammary epithelial cells

C:Genetics:

A:Gene: GDB:DUSP5

A:Cross-references: GDB:385447

A:Map position: 10q25-10q25

C:Superfamily: dual specificity phosphoprotein phosphatase 1; Vhl-type dual specificity

C:Keywords: phosphoprotein; phosphoric monoester hydrolase

F:186-317/Domain: Vhl-type dual specificity phosphoprotein phosphatase homology <VH1>

F:265/Active site: Cys (phosphocysteine intermediate) #status predicted

F:269/Binding site: substrate phosphate (Arg) #status predicted

Query Match 22.7%; Score 221.5; DB 1; Length 384;

Best Local Similarity 36.5%; Pred. No. 2.4e-13;

Matches 50; Conservative 29; Mismatches 57; Indels 1; Gaps 1;

Qy 4 GNMKILPGLYIGNFKDARDABQLSKNKVTHTLSV-HDSARPMLEGVKYLICIPAADSPSQN 62

Db 178 GPVEILPPLVLSAVHASKCEFLANLHITALLNVSRRTSSEACMTHLVKPIWVEDSHTD 237

Qy 63 LTRFKESIKFIHECRLRGESCLVHCLAGVSRVTLVIAYITMTDQWEDALHTVTRAGR 122

Db 238 ISSHFQEAIDFIDCVREKGGKVLVHCEAGISRSPTICMAYLMKTQKFLKEAFDIYIKQR 297

Qy 123 SCAMPNVGFQRLQEFKE 139

Db 298 SWVSPFNGFMQLQIYE 314

## RESULT 8

F88481

protein C16A3.1 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001

C:Accession: F88481

R:Anonymous, the C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology

A:Reference number: A75000; MUID:99069613; PMID:9851916

A:Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_eleg

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A:Accession: F88481

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-866 <STO>

A:Cross-references: GB:chr\_III; PIDN:AAB47600.1; PID:gl109830; GSPDB:GN00021; CESP:C16A3

C:Genetics:

A:Gene: C16A3.1

A:Map position: 3

Query Match 22.4%; Score 218; DB 2; Length 866;

Best Local Similarity 28.5%; Pred. No. 1.4e-12;

Matches 49; Conservative 41; Mismatches 70; Indels 12; Gaps 3;

Qy 5 MNKILPGLYIGNFKDARDABQLSKNKVTHTLSVHD-----SARPMLEGVKYLICIPAAD 57

Db 44 ISEILPNLYLSGRVTSQNSSELLKEKNITTVINVSDEVVNYKNNQKFIKNYRFYAM--SD 101

Qy 58 SPSONLTRFKESIKFIHECRLRGESCLVHCLAGVSRVTLVIAYITMTDQWEDALHT 117

Db 102 TASAKFDGIIIEAVRIIHDSRSKEEGLVHCFGLGVSRSATVAFYLSALSINNRDADF 161

Qy 118 VRAGSCAMPNVGFQRLQEFKEHVEHYQVWMLKEEYGESPLQDAEERAKNII 169

Db 162 IHRFRFSANPFGFLHQLKVTSTTAKEFRNQL---ISERCLRMRESDKDII 210

## RESULT 9

JC7885

low-molecular-mass dual-specificity phosphatase-2 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 09-Dec-2002 #sequence\_revision 09-Dec-2002 #text\_change 09-Jul-2004

C:Accession: JC7885

R:Nakamura, K.; Tanoue, K.; Satoh, T.; Takekawa, M.; Watanabe, M.; Shima, H.; Kikuchi, K.

J. Biochem. 132, 463-470, 2002

A:Title: A novel low-molecular-mass dual-specificity phosphatase, LDP-2, with a naturally

A:Reference number: JC7885; MUID:22194259; PMID:12204117

A:Accession: JC7885

A:Molecule type: mRNA

A:Residues: 1-220 <NAK>

A:Cross-references: UNIPROT:Q99N12; DDBJ:AB038769; DDBJ:AB038770

C:Comment: This enzyme, a novel member of the low-molecular-mass dual-specificity phospho

ein kinase signaling.

C:Genetics:

A:Gene: ldp-2

Query Match 21.6%; Score 210.5; DB 2; Length 220;

Best Local Similarity 36.8%; Pred. No. 1.4e-12;

Matches 49; Conservative 22; Mismatches 61; Indels 1; Gaps 1;

Qy 8 ILPLGYIGNFKDARDABQLSKNKVTHTLSV-HDSARPMLEGVKYLICIPAADSPSQNLTRH 66

Db 68 IKPMLILGSDAHDHLLRGKHTHILNVAYGVENAFLESEYTKTISILDVPETNILSY 127

Qy 67 FKESIKFIHECRLRGESCLVHCLAGVSRVTLVIAYITMTDQWEDALHTVTRAGSCAN 126

Db 128 FPECFEIEQAKDKGVVLVHCVNAGVRAAAIVGFLMSSEATFTTALSIVKEARPSIC 187

Qy 127 PNVCFQRLQEFKE 139

Db 188 PNPGFMEQLRTYQ 200

## RESULT 10

T46405  
hypothetical protein DKFZp43401321.1 - human  
C;Species: Homo sapiens (man)  
C;Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 09-Jul-2004  
C;Accession: T46405  
R;Blum, H.; Baueraachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, January 2000  
A;Reference number: Z23034  
A;Accession: T46405  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-303 <AAA>  
A;Cross-references: UNIPROT:Q9NSW1; EMBL:AL137704  
A;Experimental source: adult testis; clone DKFZp43401321  
C;Genetics:  
A;Note: DKFZp43401321.1

Query Match 20.9%; Score 203.5; DB 2; Length 303;  
Best Local Similarity 36.4%; Pred. No. 9.3e-12;  
Matches 51; Conservative 24; Mismatches 58; Indels 7; Gaps 3;  
  
Qy 4 GNMKILPGLYIGNFKDARDAEQLSKNKKVTHILSVHDSARPMLLEG-VKYLCTIPAADSPSQN 62  
Db 104 GPVEILPFLYLGSAVHAARRDMLDALGITALLNVSSDCPNHFEGHYQYKCIPIVEDNHKAD 163  
Qy 63 LTRHFKESIKFI---HECRLRGESCLVHCLAGVRSVTLVIAYIMTVTDFGWDALHTVR 119  
Db 164 ISSWFMEALIEYIDAVKDCRGR---VLVHCQAGISRSATICLAYLMMKKRVRLLEAFEFVK 220  
Qy 120 AGRSCANPNVGFQRLQEF 139  
Db 221 QRRSIISPNFSFMGQLLQFE 240

## RESULT 11

A56947  
dual specificity phosphatase (EC 3.1.3.-) HVH2 - rat  
N;Alternate names: mitogen-activated protein kinase phosphatase 2  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 17-Mar-1999  
C;Accession: A56947  
R;Miyara-Press, A.; Rim, C.S.; Yao, H.; Robertson, M.S.; Stork, P.J.S.  
J. Biol. Chem. 270, 14587-14596, 1995  
A;Title: A novel mitogen-activated protein kinase phosphatase. Structure, expression, and  
A;Reference number: A56947; MUID:95301550; PMID:7782322  
A;Accession: A56947  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-393 <MTS>

C;Superfamily: dual specificity phosphoprotein phosphatase 1; VH1-type dual specificity  
C;Keywords: phosphoprotein; phosphoric monoester hydrolase  
F;202-333/Domain: VH1-type dual specificity phosphoprotein phosphatase homology <VH1>  
F;279/Active site: Cys (phosphocysteine intermediate) #status predicted  
F;295/Binding site: substrate phosphate (Arg) #status predicted

Query Match 20.9%; Score 203.5; DB 2; Length 393;  
Best Local Similarity 36.4%; Pred. No. 1.3e-11;  
Matches 51; Conservative 24; Mismatches 58; Indels 7; Gaps 3;  
  
Qy 4 GNMKILPGLYIGNFKDARDAEQLSKNKKVTHILSVHDSARPMLLEG-VKYLCTIPAADSPSQN 62  
Db 194 GPVEILPFLYLGSAVHAARRDMLDALGITALLNVSSDCPNHFEGHYQYKCIPIVEDNHKAD 253  
Qy 63 LTRHFKESIKFI---HECRLRGESCLVHCLAGVRSVTLVIAYIMTVTDFGWDALHTVR 119  
Db 254 ISSWFMEALIEYIDAVKDCRGR---VLVHCQAGISRSATICLAYLMMKKRVRLLEAFEFVK 310  
Qy 120 AGRSCANPNVGFQRLQEF 139  
Db 311 QRRSIISPNFSFMGQLLQFE 330

## RESULT 12

T03074  
dual specificity phosphoprotein phosphatase homolog - Chilo iridescent virus  
C;Species: Chilo iridescent virus  
C;Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 09-Jul-2004  
C;Accession: T03074  
R;Bahr, U.; Tidona, C.A.; Darai, G.  
Virus Genes 15, 235-245, 1997  
A;Title: The DNA sequence of Chilo iridescent virus between the genome coordinates 0.101  
A;Reference number: Z14834; MUID:98141693; PMID:9482589  
A;Accession: T03074  
A;Status: preliminary; translated from GB/EMBL/DBDJB  
A;Molecule type: DNA  
A;Residues: 1-142 <BAH>  
A;Cross-references: UNIPROT:O55737; EMBL:AF003534; NID:G2738385; PIDN:AAB94448.1; PID:G2738385

Query Match 20.7%; Score 201.5; DB 2; Length 142;  
Best Local Similarity 33.3%; Pred. No. 5.8e-12;  
Matches 48; Conservative 25; Mismatches 58; Indels 13; Gaps 2;  
  
Qy 7 KIILPGLYIGNFKDARDAEQLSKNKKVTHILSVHDSARPMLLEGVKYLCTIPAADSPSQNLTRH 66  
Db 5 KIVENLYLGNIGIRHSNYGFDKIINLTRENNQ-----YCIPTVWINIDDSSESDLYSH 59  
Qy 67 FKESIKFIHECRLRGESCLVHCLAGVRSVTLVIAYIMTVTDFGWDALHTVRAGRSKAN 126  
Db 60 LQKVTTLIHDSIENGKVLVHCQAGISRSATVVIAYIMRSKRYSLQDAFNFVKKRSLIF 119  
Qy 127 PNVGFQRLQEFKEGHEVHYQYRWL 150  
Db 120 PNAGFIKQLAQFER-----WL 135

## RESULT 13

A56115  
dual specificity phosphoprotein phosphatase (EC 3.1.3.-) 4 - human  
N;Alternate names: dual specificity phosphatase HVH2  
C;Species: Homo sapiens (man)  
C;Date: 19-Oct-1995 #sequence\_revision 19-Oct-1995 #text\_change 09-Jul-2004  
C;Accession: A56115  
R;Guan, K.L.; Butch, E.  
J. Biol. Chem. 270, 7197-7203, 1995  
A;Title: Isolation and characterization of a novel dual specific phosphatase, HVH2, which  
A;Reference number: A56115; MUID:95221370; PMID:7535768  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-394 <GUA>  
A;Cross-references: UNIPROT:Q13649; GB:U21108  
C;Genetics:

A;Gene: GDB:DUSP4; HVH2; MKP-2  
A;Cross-references: GDB:433893  
C;Map position: 9p21-8p11.2  
C;Superfamily: dual specificity phosphoprotein phosphatase 1; VH1-type dual specificity  
C;Keywords: phosphoprotein; phosphoric monoester hydrolase  
F;203-334/Domain: VH1-type dual specificity phosphoprotein phosphatase homology <VH1>  
F;280/Active site: Cys (phosphocysteine intermediate) #status predicted  
F;286/Binding site: substrate phosphate (Arg) #status predicted

Query Match 20.7%; Score 201.5; DB 2; Length 394;  
Best Local Similarity 36.4%; Pred. No. 2e-11;  
Matches 51; Conservative 23; Mismatches 59; Indels 7; Gaps 3;  
  
Qy 4 GNMKILPGLYIGNFKDARDAEQLSKNKKVTHILSVHDSARPMLLEG-VKYLCTIPAADSPSQN 62  
Db 195 GPVEILPFLYLGSAVHAARRDMLDALGITALLNVSSDCPNHFEGHYQYKCIPIVEDNHKAD 254  
Qy 63 LTRHFKESIKFI---HECRLRGESCLVHCLAGVRSVTLVIAYIMTVTDFGWDALHTVR 119  
Db 255 ISSWFMEALIEYIDAVKDCRGR---VLVHCQAGISRSATICLAYLMMKKRVRLLEAFEFVK 311  
Qy 120 AGRSCANPNVGFQRLQEF 139

Db 312 QRRSIISPNFSGQLLOFE 331

## RESULT 14

A57126

dual specificity phosphoprotein phosphatase (EC 3.1.3.-) 2 - human  
N:Alternate names: mitogen-induced nuclear tyrosine phosphatase; phosphatase of activate  
C:Species: Homo sapiens (man)  
C:Date: 03-Nov-1995 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: A57126

R:Rohan, P.J.; Davis, P.; Moekaluk, C.A.; Kearns, M.; Krutzsch, H.; Siebenlist, U.; Kell  
Science 259, 1763-1766, 1993  
A:Title: PAC-1: a mitogen-induced nuclear protein tyrosine phosphatase.

A:Reference number: A57126; MUID:93206122; PMID:7681221

A:Accession: A57126

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-314 <ROH>

A:Cross-references: UNIPROT:Q05923; GB:L111329; NID:9559539; PIDN:AAA50779.1; PID:g292376

C:Genetics:

A:Gene: GDB:DUSP2

A:Cross-references: GDB:139200

A:Map position: 2q11-2q11

C:Function:

A:Description: catalyzes the hydrolysis of peptidyl-phosphoserine, -phosphothreonine, and  
C:Superfamily: dual specificity phosphoprotein phosphatase 1; VHI-type dual specificity  
C:Keywords: nucleus; phosphoprotein; phosphoric monoester hydrolase

F:140-160/Region: nuclear location signal

F:180-311/Domain: VHI-type dual specificity phosphoprotein phosphatase homology <VHI>

F:257/Active site: Cys (phosphocysteine intermediate) #status predicted

F:263/Binding site: substrate phosphate (Arg) #status predicted

Query Match 20.1%; Score 195.5; DB 1; Length 314;

Best Local Similarity 34.3%; Pred. No. 5.6e-11;

Matches 47; Conservative 26; Mismatches 63; Indels 1; Gaps 1;

Qy 4 GNMKILPGLYIGNFKDARDAEQLSKNKTHTLSVHDSARPMLGV-KYLCTIPAADSPSQN 62

Db 172 GPVEILPYFLGSGSHSSDLQGLQACGITAIVLNVSASCPNHFEGLYRYSIPVEDNQMV 231

Qy 63 LTRHFKESIKPIHECRLRGSCLVHCLAGVSRVTLVIAYIMTVTDFGWEDALHTVRAGR 122

Db 232 ISAWFQEAIGFDWYKNSGGRLVHCQAGISRSATICLAYLMQRRLDEAFDFVKQR 291

Qy 123 SCANPNVGFQRLQOFE 139

Db 292 GVISPNFSGQLLOFE 308

## RESULT 15

S29090

dual specificity phosphoprotein phosphatase (EC 3.1.3.-) 1 - human  
N:Alternate names: protein-tyrosine-phosphatase CL100; protein-tyrosine-phosphatase, non  
C:Species: Homo sapiens (man)

C:Date: 25-Feb-1994 #sequence\_revision 02-May-1994 #text\_change 09-Jul-2004

C:Accession: S29090; A53052

R:Keyse, S.M.; Emalie, E.A.

Nature 359, 644-647, 1992

A:Title: Oxidative stress and heat shock induce a human gene encoding a protein-tyrosine

A:Reference number: S29090; MUID:93024952; PMID:1406996

A:Accession: S29090

A:Molecule type: mRNA

A:Residues: 1-367 <KEY>

A:Cross-references: UNIPROT:P28562; EMBL:X68277; NID:g29980; PIDN:CAA48338.1; PID:g29981

R:Kwak, S.P.; Hakes, D.J.; Martell, K.J.; Dixon, J.E.

J. Biol. Chem. 269, 3596-3604, 1994

A:Title: Isolation and characterization of a human dual specificity protein-tyrosine pho

A:Reference number: A53052; MUID:94148864; PMID:8106404

A:Accession: A53052

A:Molecule type: DNA

A:Residues: 1-367 <KWA>

A:Experimental source: leukocyte

A:Note: sequence extracted from NCBI backbone (NCBIN:143800, NCBIN:143802, NCBIN:143804,

C:Genetics:

A:Gene: GDB:DUSP1; PTFN10

A:Cross-references: GDB:l36197; OMIM:600714

A:Map position: 5q34-5q34

C:Superfamily: dual specificity phosphoprotein phosphatase 1; VHI-type dual specificity  
C:Keywords: heat shock; phosphoprotein; phosphoric monoester hydrolase; stress-induced p  
F:181-312/Domain: VHI-type dual specificity phosphoprotein phosphatase homology <VHI>  
F:258/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:264/Binding site: substrate phosphate (Arg) #status predicted

Query Match 19.9%; Score 194.5; DB 1; Length 367;

Best Local Similarity 33.6%; Pred. No. 8.4e-11;

Matches 46; Conservative 25; Mismatches 65; Indels 1; Gaps 1;

Qy 4 GNMKILPGLYIGNFKDARDAEQLSKNKTHTLSVHDSARPMLGV-KYLCTIPAADSPSQN 62

Db 173 GPVEILPYFLGSAHYASRKDMLDGLITALINVSANCPNHFEGHYQKYSIPVEDNHKAD 232

Qy 63 LTRHFKESIKPIHECRLRGSCLVHCLAGVSRVTLVIAYIMTVTDFGWEDALHTVRAGR 122

Db 233 ISSWFNEAIDFIDSINKAGGRVHVHCQAGISRSATICLAYLMRTNRVVKLDEAFDFVKQR 292

Qy 123 SCANPNVGFQRLQOFE 139

Db 293 SIISPNFSGQLLOFE 309

Search completed: July 21, 2005, 19:03:32

Job time : 66 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 21, 2005, 18:56:44 ; Search time 91 Seconds  
(without alignments)  
150,939 Million cell updates/sec

Title: US-10-658-661-2

Perfect score: 975

Sequence: 1 MGNMKNILPGLYIGNFKDA.....AKNIIAAPGILKFWAFLLRL 184

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA\*

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- 2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	246.5	25.3	170	4	US-09-557-921-14
2	246.5	25.3	482	4	US-09-557-921-2
3	245.5	25.2	421	4	US-09-949-016-10488
4	245	25.1	207	4	US-09-270-767-44103
5	244.5	25.1	156	4	US-09-955-732A-3
6	244.5	25.1	170	4	US-09-544-716-12
7	244.5	25.1	170	4	US-09-557-921-12
8	244.5	25.1	170	4	US-09-564-357-15
9	244.5	25.1	170	4	US-09-619-380-14
10	244.5	25.1	491	4	US-09-949-016-8486
11	243.5	25.0	156	4	US-09-955-732A-5
12	234	24.0	223	4	US-09-685-833A-2
13	234	24.0	223	4	US-09-816-494-5
14	233.5	23.9	156	4	US-09-955-732A-4
15	233.5	23.9	168	4	US-09-544-716-13
16	233.5	23.9	168	4	US-09-557-921-13
17	233.5	23.9	168	4	US-09-564-357-16
18	233.5	23.9	168	4	US-09-619-380-15
19	228.5	23.4	659	4	US-09-955-732A-2
20	225.5	23.1	471	4	US-09-955-732A-21
21	225	23.1	172	4	US-09-704-139-5
22	225	23.1	172	4	US-09-816-494-8
23	221.5	22.7	154	4	US-09-955-732A-10
24	221.5	22.7	171	4	US-09-544-716-18
25	221.5	22.7	171	4	US-09-557-921-19
26	221.5	22.7	171	4	US-09-564-357-21
27	221.5	22.7	171	4	US-09-619-380-20

28	221.5	22.7	210	4	US-09-949-016-10939	Sequence 10939, A
29	221.5	22.7	384	4	US-09-949-016-6494	Sequence 6494, Ap
30	221.5	22.7	397	2	US-08-990-379-8	Sequence 8, Appli
31	220	22.6	155	4	US-09-955-732A-6	Sequence 6, Appli
32	220	22.6	170	4	US-09-544-716-14	Sequence 14, Appl
33	220	22.6	170	4	US-09-557-921-15	Sequence 15, Appl
34	220	22.6	170	4	US-09-564-357-17	Sequence 17, Appl
35	220	22.6	170	4	US-09-619-380-16	Sequence 16, Appl
36	220	22.6	661	4	US-09-949-016-9121	Sequence 9121, Ap
37	217.5	22.3	283	4	US-09-270-767-45300	Sequence 45300, A
38	217.5	22.3	737	4	US-09-955-732A-13	Sequence 13, Appl
39	216.5	22.2	173	4	US-09-704-139-4	Sequence 4, Appli
40	216.5	22.2	173	4	US-09-816-494-7	Sequence 7, Appli
41	212	21.7	174	4	US-09-544-716-20	Sequence 20, Appl
42	212	21.7	211	4	US-09-544-716-2	Sequence 2, Appli
43	210.5	21.6	552	4	US-09-955-732A-15	Sequence 15, Appl
44	208	21.3	665	4	US-09-816-494-2	Sequence 2, Appli
45	206.5	21.2	299	4	US-09-564-357-4	Sequence 4, Appli

## ALIGNMENTS

### RESULT 1

US-09-557-921-14  
; Sequence 14, Application US/09557921  
; Patent No. 6551810  
; GENERAL INFORMATION:  
; APPLICANT: Luche, Ralf M.  
; APPLICANT: Wei, Bo  
; TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE  
; FILE REFERENCE: 200125.416  
; CURRENT APPLICATION NUMBER: US/09/557,921  
; CURRENT FILING DATE: 2000-04-20  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 170  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-557-921-14

Query Match 25.3%; Score 246.5; DB 4; Length 170;  
Best Local Similarity 38.6%; Pred. No. 4.2e-22;  
Matches 54; Conservative 29; Mismatches 52; Indels 5; Gaps 2;

Qy	5	MNKLPGLYIGNFKDADAEOLSKNKHVTHLSVHDSARPMLEGVK----	YLCIPADSPS 60
Db	27	LTPLPFLFLGNEQDAQDLTMQRLNIGYVINV-TTHPLHYHKEKGLFNFKRLPATDSNK 85	
Qy	61	QNLTRHFKESIKFTHECRGESCIVHCLAGSVSVTLVIAYIMTVTDFGHEDALHTVRA 120	
Db	86	QNLQYFEAEFEETEAHQCGKGLLIHCQAGVRSATIVIAIYLMKHTMTWTDAYKFKVG 145	
Qy	121	GRSCANPNVGFQRLQEFEK 140	
Db	146	KRPIISNPNLPMGQLLEFEE 165	

### RESULT 2

US-09-557-921-2  
; Sequence 2, Application US/09557921  
; Patent No. 6551810  
; GENERAL INFORMATION:  
; APPLICANT: Luche, Ralf M.  
; APPLICANT: Wei, Bo  
; TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE  
; FILE REFERENCE: 200125.416  
; CURRENT APPLICATION NUMBER: US/09/557,921  
; CURRENT FILING DATE: 2000-04-20  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2

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; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-557-921-2

Query Match      25.3%; Score 246.5; DB 4; Length 482;
Best Local Similarity 38.6%; Pred. NO. 2.1e-21;
Matches 54; Conservative 29; Mismatches 52; Indels 5; Gaps 2;

QY      5 MNKIPLGLYIGNFKDARDAEQLSKNKKVTHILSVHDSARPMLGVK----YLCIPAAADSPS 60
Db      322 LTPILPFLFELGNEQAQDLDTMQLNLNIGYLVN--TTHPLYHYEKGFLFNKRLPATDSNK 380

QY      61 QNLTRHFKEIKFIHECKLRGESCILVHCLAGVRSVTLVIAYIMTVDTFGWEDALHTVRA 120
Db      381 QNLQVFEAEFIEAHQCGKGLLIHQAGVRSATIVIALMKHTRMTMTDAYKFKVG 440

QY      121 GRSCANPVGFQRLQEFK 140
Db      441 KRPIISPNLNFMGOLLEFEE 460

RESULT 3
US-09-949-016-10488
; Sequence 10488, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10488
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10488

Query Match      25.2%; Score 245.5; DB 4; Length 421;
Best Local Similarity 39.6%; Pred. NO. 2.2e-21;
Matches 59; Conservative 24; Mismatches 59; Indels 7; Gaps 2;

QY      7 KTLPLGLYIGNFKDARDAEQLSKNKKVTHILSVHDSARPMLV---GVKLCIPAAADSPQNL 63
Db      243 QILPNLYLSAEDSANTLESALKLGIRYILNTVPLNPFNFKEKNGDFHYKQIPISDHWSQL 302

QY      64 TRHFKEIKFIHECKLRGESCILVHCLAGVRSVTLVIAYIMTVDTFGWEDALHTVRAGRS 123
Db      303 SRFFPEAEFIDEALSQNGVLVHCLAGVRSVTVVAYLMQKLHLISLNDAYDLVKKKS 362

QY      124 CANPNVGFQRLQEFK----HEVHQYRQ 148
Db      363 NISPNFMFGQLDFERSLRLERHSQEQ 391

RESULT 4
US-09-270-767-44103
; Sequence 44103, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767

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; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-544-716-12

Query Match      25.1%; Score 244.5; DB 4; Length 170;
Best Local Similarity 41.0%; Pred. No. 7.5e-22;
Matches 57; Conservative 27; Mismatches 48; Indels 7; Gaps 3;

Qy 7 KILPGLYGNFKDARDAEQLSKNKTHTLSVHDSARPMLGV---KYLCPAADSPSQNL 63
Db 28 EILPFLYLGCAKDSNLDVLEEFGIKYLNTVTPNLPNLFENAGFKYKQIPISDHSQNL 87
Qy 64 TRHPKESIKFTHECKLRGESC--LVHCLAGVSRSTVLVIAYIMTVTDGWDALHTVRAG 121
Db 88 SQFPEAISFIDEA--RGKNCGLVHCLAGISRSVTVTVAIYLMQKLNLSMNDAYDIVKMK 145
Qy 122 RSCANPNVGFQRLQOEPEK 140
Db 146 KSNISPNFNFMGQLLDFER 164

RESULT 7
US-09-557-921-12
; Sequence 12, Application US/09557921
; Patent No. 6551810
; GENERAL INFORMATION:
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.416
; CURRENT APPLICATION NUMBER: US/09/557,921
; CURRENT FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-557-921-12

Query Match      25.1%; Score 244.5; DB 4; Length 170;
Best Local Similarity 41.0%; Pred. No. 7.5e-22;
Matches 57; Conservative 27; Mismatches 48; Indels 7; Gaps 3;

Qy 7 KILPGLYGNFKDARDAEQLSKNKTHTLSVHDSARPMLGV---KYLCPAADSPSQNL 63
Db 28 EILPFLYLGCAKDSNLDVLEEFGIKYLNTVTPNLPNLFENAGFKYKQIPISDHSQNL 87
Qy 64 TRHPKESIKFTHECKLRGESC--LVHCLAGVSRSTVLVIAYIMTVTDGWDALHTVRAG 121
Db 88 SQFPEAISFIDEA--RGKNCGLVHCLAGISRSVTVTVAIYLMQKLNLSMNDAYDIVKMK 145
Qy 122 RSCANPNVGFQRLQOEPEK 140
Db 146 KSNISPNFNFMGQLLDFER 164

RESULT 8
US-09-564-357-15
; Sequence 15, Application US/09564357
; Patent No. 6645753
; GENERAL INFORMATION:
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-5 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.413
; CURRENT APPLICATION NUMBER: US/09/564,357
; CURRENT FILING DATE: 2000-04-24
; NUMBER OF SEQ ID NOS: 22

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-564-357-15

Query Match      25.1%; Score 244.5; DB 4; Length 170;
Best Local Similarity 41.0%; Pred. No. 7.5e-22;
Matches 57; Conservative 27; Mismatches 48; Indels 7; Gaps 3;

Qy 7 KILPGLYGNFKDARDAEQLSKNKTHTLSVHDSARPMLGV---KYLCPAADSPSQNL 63
Db 28 EILPFLYLGCAKDSNLDVLEEFGIKYLNTVTPNLPNLFENAGFKYKQIPISDHSQNL 87
Qy 64 TRHPKESIKFTHECKLRGESC--LVHCLAGVSRSTVLVIAYIMTVTDGWDALHTVRAG 121
Db 88 SQFPEAISFIDEA--RGKNCGLVHCLAGISRSVTVTVAIYLMQKLNLSMNDAYDIVKMK 145
Qy 122 RSCANPNVGFQRLQOEPEK 140
Db 146 KSNISPNFNFMGQLLDFER 164

RESULT 9
US-09-619-380-14
; Sequence 14, Application US/09619380
; Patent No. 6649391
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; TITLE OF INVENTION: DSP-11 DUAL SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.418
; CURRENT APPLICATION NUMBER: US/09/619,380
; CURRENT FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-619-380-14

Query Match      25.1%; Score 244.5; DB 4; Length 170;
Best Local Similarity 41.0%; Pred. No. 7.5e-22;
Matches 57; Conservative 27; Mismatches 48; Indels 7; Gaps 3;

Qy 7 KILPGLYGNFKDARDAEQLSKNKTHTLSVHDSARPMLGV---KYLCPAADSPSQNL 63
Db 28 EILPFLYLGCAKDSNLDVLEEFGIKYLNTVTPNLPNLFENAGFKYKQIPISDHSQNL 87
Qy 64 TRHPKESIKFTHECKLRGESC--LVHCLAGVSRSTVLVIAYIMTVTDGWDALHTVRAG 121
Db 88 SQFPEAISFIDEA--RGKNCGLVHCLAGISRSVTVTVAIYLMQKLNLSMNDAYDIVKMK 145
Qy 122 RSCANPNVGFQRLQOEPEK 140
Db 146 KSNISPNFNFMGQLLDFER 164

RESULT 10
US-09-949-016-8486
; Sequence 8486, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20

```

```
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR PUBLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8486
; LENGTH: 491
; TYPE: PRP
; ORGANISM: Human
US-09-949-016-8486

Query Match      25.1%; Score 244.5; DB 4; Length 491;
Best Local Similarity 41.0%; Pred. No. 3.8e-21;
Matches 57; Conservative 27; Mismatches 48; Indels 7; Gaps 3

QY    7 KILPLGIYNFKDARDAEQLSKNVKTHILLSVHDSARPMLGV--KYLCIPAAADSPSQNL 63
DB   319 EILPFLYGCAKOSTNLDLVEFGIKYLNTPNLPNFENAGEFKKYKIPISDHWSQL 378
      :|::|||:|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY    64 TRHKESIKFHCRLRGESC--LVHCLGAVSRSVTVLIAYIMVTDFGWEDALHTVRAG 121
DB   379 SQPFPEAISFIDEA-RGKNCGVLHVCHLAGISRSVTIVAYLMQMKLNSMNDAYDIVGMK 436
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY   122 RSCANPNVGFORLOEFEK 140
DB   437 KSNISPNNFMGQLLDFER 455
      :|::|||:|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 11
US-09-955-732A-5
; Sequence 5, Application US/09955732A
; Patent No. 6825021
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.433
; CURRENT APPLICATION NUMBER: US/09/955,732A
; CURRENT FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 156
; TYPE: PRP
; ORGANISM: Homo sapiens
US-09-955-732A-5

Query Match      25.0%; Score 243.5; DB 4; Length 156;
Best Local Similarity 40.9%; Pred. No. 8.7e-22;
Matches 56; Conservative 24; Mismatches 54; Indels 3; Gaps 1

QY    7 KILPLGIYNFKDARDAEQLSKNVKTHILLSVHDSARPMLE---GVKYLCIPAAADSPSQNL 63
DB   15 QILPNLYGSARDSANLESIAKGIRIYLTNPINPFNKNGDPHYKQIPISDHWSQL 74
      :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY    64 TRHKESIKFHCRLRGESCCLVHCLGAVSRSVTVLIAYIMVTDFGWEDALHTVRGRS 123
DB   75 SRFPFEAIETFDALSQCNGCVLHVCHLAGISRSVTITVAIYMQLHLSDLNDAYDLVKRKS 134
      :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY   124 CANPNVGFORLOEFEK 140
DB   135 NISFNFMGQLLDFER 151
      :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 12
US-09-685-853A-2
; Sequence 2, Application US/09685853A
; Patent No. 6479270
; GENERAL INFORMATION:
; APPLICANT: Wei, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
; NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,
```

```

; GENERAL INFORMATION:
; APPLICANT: Lucche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.433
; CURRENT APPLICATION NUMBER: US/09/955,732A
; CURRENT FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-955-732A-4

Query Match      23.9%; Score 233.5; DB 4; Length 156;
Best Local Similarity 40.1%; Pred. No. 1.5e-20;
Matches 55; Conservative 24; Mismatches 55; Indels 3; Gaps 1;

QY 7 KILPGLYIGNFKDARDAEQLSKNKKVTHILSVHDSARPML---GVKYLICIPAADSPSONL 63
Db 15 QILPYLYLGCAKDNLDVLGKYGKIKYILNVTPLNPNAFEHGGEFTYKQIPISDHWSQNL 74
QY 64 TRHFKEIKFTHIECLRGESCLVHCLAGVSRVTLVIAYIMTVDFGWEDALHTVTRAGRS 123
Db 75 SQFFPEAISFIDEARSKCGVLVHCLAGISRSVTVVAYLMQKNLNLNDAYDFVKRKKS 134
QY 124 CANPNVGFQRLQEFEK 140
Db 135 NISPNFNFQQLDPER 151

```

```

RESULT 15
US-09-544-716-13
; Sequence 13, Application US/09544716
; Patent No. 6492157
; GENERAL INFORMATION:
; APPLICANT: Lucche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-9 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.415
; CURRENT APPLICATION NUMBER: US/09/544,716
; CURRENT FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-544-716-13

```

```

Query Match      23.9%; Score 233.5; DB 4; Length 168;
Best Local Similarity 40.1%; Pred. No. 1.7e-20;
Matches 55; Conservative 24; Mismatches 55; Indels 3; Gaps 1;

QY 7 KILPGLYIGNFKDARDAEQLSKNKKVTHILSVHDSARPML---GVKYLICIPAADSPSONL 63
Db 26 QILPYLYLGCAKDNLDVLGKYGKIKYILNVTPLNPNAFEHGGEFTYKQIPISDHWSQNL 85
QY 64 TRHFKEIKFTHIECLRGESCLVHCLAGVSRVTLVIAYIMTVDFGWEDALHTVTRAGRS 123
Db 86 SQFFPEAISFIDEARSKCGVLVHCLAGISRSVTVVAYLMQKNLNLNDAYDFVKRKKS 145
QY 124 CANPNVGFQRLQEFEK 140
Db 146 NISPNFNFQQLDPER 162

```

Search completed: July 21, 2005, 19:25:06  
Job time : 91 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 21, 2005, 15:47:20 ; Search time 275 Seconds  
(without alignments)  
258.778 Million cell updates/sec

Title: US-10-658-661-2

Perfect score: 975

Sequence: 1 MGNMGKILPLGLYIGNFKDA.....AKNLAAPGILKFWAFLRL 184

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_16Dec04:\*

1: Geneseq1980s:\*

2: Geneseq1990s:\*

3: Geneseq2000s:\*

4: Geneseq2001s:\*

5: Geneseq2002s:\*

6: Geneseq2003as:\*

7: Geneseq2003bs:\*

8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	975	100.0	184	3	Aay68795 Amino aci
2	975	100.0	184	4	AAB73216 Human pho
3	975	100.0	184	4	AAB66431 Human DSP
4	975	100.0	184	4	AAG78217 Human MAP
5	975	100.0	184	4	AAB67167 Human dua
6	975	100.0	184	5	ABE90435 Human pol
7	975	100.0	184	5	ADI16892 Human NOV
8	975	100.0	184	5	ADI17160 Human NOV
9	975	100.0	184	6	ABR43223 Human mit
10	975	100.0	184	7	ADH89787 Human MKP
11	975	100.0	184	8	ADN75954 Human sig
12	975	100.0	184	8	ADP25001 PRO polyp
13	975	100.0	190	4	AAU23521 Novel hum
14	975	100.0	190	4	AAU21668 Novel hum
15	975	100.0	190	4	AAU21796 Novel hum
16	975	100.0	190	7	ADC46309 Human neo
17	975	100.0	190	7	ADC46437 Human neo
18	959	98.4	184	6	ABR43457 Human dua
19	932	95.6	184	4	AAB73213 Murine ph
20	932	95.6	184	5	ADI17161 Murine NO
21	932	95.6	184	5	ADI16893 Murine NO
22	923	94.7	184	5	ADI16894 Human NOV
23	923	94.7	184	5	ADI17162 Human NOV
24	897	92.0	205	4	AAB81105 Human JNK
25	856	87.8	205	4	AAB66443 Murine DS

26	843	86.5	205	4	AAB81106	Aab81106 Murine JN
27	825.5	84.7	167	3	AAB23298	Aab23298 Human dua
28	758.5	77.8	145	3	AAB66442	Aab66442 Human MAP
29	673	69.0	162	7	ADB65317	Adb65317 Human pro
30	540	55.4	122	4	AAU23718	Aau23718 Novel hum
31	528	54.2	235	5	AAE22996	Aae22996 Human pro
32	528	54.2	235	5	ADI16890	Adi16890 Human NOV
33	528	54.2	235	5	ADI17159	Adi17159 Human NOV
34	528	54.2	235	6	ABR43456	Abr43456 Human dua
35	528	54.2	235	6	ABR43461	Abr43461 Human DSP
36	528	54.2	235	8	ADN76006	Adn76006 Human DSP
37	528	54.2	235	8	ADN75958	Adn75958 Human sig
38	528	54.2	289	5	AAE22997	Aae22997 Human pro
39	528	54.2	289	6	ABR43462	Abr43462 Human DSP
40	528	54.2	329	4	AAE04840	Aae04840 Human SGP
41	528	54.2	329	5	AAU75792	Aau75792 Human pro
42	528	54.2	329	6	ABR43460	Abr43460 Human DSP
43	521	53.4	236	5	ADI16572	Adi16572 Human NOV
44	512	52.5	236	8	ADN42226	Adn42226 Human nov
45	483.5	49.6	149	6	ABR43466	Abr43466 Multiple

## ALIGNMENTS

### RESULT 1

AAy68795  
ID AAY68795 standard; protein; 184 AA.

XX AC AAY68795;

XX AC 16-MAY-2000 (first entry)

XX DT Amino acid sequence of a human phosphorylation effector PHSP-27.

XX DE Human; phosphorylation effector; PHSP; proliferative disorder; immune disorder; neuronal disorder.

XX KW Homo sapiens.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Modified-site 36 /note= "potential phosphorylation domain"

FT Modified-site 40 /note= "potential phosphorylation domain"

FT Modified-site 50 /note= "potential phosphorylation domain"

FT Modified-site 62 /note= "potential glycosylation domain"

FT Domain 63..118 /note= "tyrosine phosphatase active site domain"

FT Modified-site 70 /note= "potential phosphorylation domain"

FT Modified-site 105 /note= "potential phosphorylation domain"

FT Modified-site 117 /note= "potential phosphorylation domain"

XX WO200006728-A2.

XX PD 10-FEB-2000.

XX PF 28-JUL-1999; 99WO-US017132.

XX PR 28-JUL-1998; 98US-0155213P.

XX PR 14-SEP-1998; 98US-0155196P.

XX PR 14-OCT-1998; 98US-0155239P.

XX PR 03-NOV-1998; 98US-0106889P.

XX PR 19-NOV-1998; 98US-0109033P.

XX PR 22-DEC-1998; 98US-0113796P.

XX PR 12-JAN-1999; 99US-0155233P.

XX PA (INCY-) INCYTE PHARM INC.

XX Hillman JL, Lal P, Tang YT, Corley NC, Guegler KJ, Baughn MR;  
 PI Patterson C, Bandman O, Au-Young J, Gorgone GA, Yue H, Azimzai Y;  
 PI Reddy R, Lu DAM, Shih LL;  
 XX WPI; 2000-183125/16.  
 DR N-PSDB; AAZ46164.  
 XX New human phosphorylation effectors useful for the diagnosis, treatment  
 PT and prevention of proliferative, immune and neuronal disorders.  
 XX  
 PS Claim 1; Page 114-115; 142pp; English.  
 XX  
 CC AAY68769-95 and AAY68797-99 represent human phosphorylation effectors  
 CC (PHSP), designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not  
 CC given in the specification). The sequences were isolated from cDNA  
 CC libraries prepared from various human tissues. The PHSP proteins are  
 CC useful for the diagnosis, treatment and prevention of proliferative  
 CC disorders, immune disorders and neuronal disorders. The PHSP proteins  
 CC form pharmaceutical compositions which useful for treating or preventing  
 CC disorders associated with decreased PHSP expression/activity. PHSP  
 CC antagonists are useful for treating or preventing disorders associated  
 CC with increased PHSP expression/activity  
 XX  
 SQ Sequence 184 AA;  
 Query Match 100.0%; Score 975; DB 3; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-108;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNGMKNKILPGLYIGNFKDARDAEQLSKNKTHTLSVHDSARPMLGKVKLCIPADSPS 60  
 DB 1 MNGMKNKILPGLYIGNFKDARDAEQLSKNKTHTLSVHDSARPMLGKVKLCIPADSPS 60  
 QY 61 QNLTTRHFKESTKFTHECRLGESCLVHCLAGVRSVTLVIAYIMTVTDFGWEDALHTVRA 120  
 DB 61 QNLTTRHFKESTKFTHECRLGESCLVHCLAGVRSVTLVIAYIMTVTDFGWEDALHTVRA 120  
 QY 121 GRSCANPNVGFQRLQEFKEHVEHQYRWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180  
 DB 121 GRSCANPNVGFQRLQEFKEHVEHQYRWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180  
 QY 181 LRRL 184  
 DB 181 LRRL 184  
 RESULT 2  
 AAB73216  
 ID AAB73216 standard; protein; 184 AA.  
 AC AAB73216;  
 XX  
 DT 11-MAY-2001 (first entry)  
 XX  
 DE Human phosphatase AA374753\_h.  
 XX  
 KW Phosphatase; gene therapy; enzyme; cancer; pathophysiological hypoxia;  
 KW cardiac dysfunction; vascular disorder; myopathy; ectodermal dysplasia;  
 KW congenital muscle disorder; Papillon-Lefevre syndrome; Cowden disease;  
 KW Moebius syndrome; Bjornstad syndrome; Bannayan Zonana syndrome;  
 KW schizophrenia; hamartoma.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200112819-A2. NPA  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 11-AUG-2000; 2000WO-US022158.  
 XX  
 PR 13-AUG-1999; 99US-0149005P.  
 XX

PA (SUGE-) SUGEN INC.  
 XX Plowman GD, Martinez R, Whyte D, Hill R, Flanagan P, Lioubin M;  
 XX N-PSDB; AAF63568.  
 DR WPI; 2001-211226/21.  
 DR N-PSDB; AAF63568.  
 XX New protein phosphatase polypeptide for diagnosing and treating  
 PT phosphatase related disorders such as cancer, schizophrenia, cardiac  
 PT dysfunction and/or vascular disorders.  
 XX  
 PS Claim 6; Fig 5; 138pp; English.  
 XX  
 CC The present invention relates to phosphatase proteins and coding  
 CC sequences. The present sequence is one such phosphatase. Phosphatases are  
 CC enzymes that catalyze the dephosphorylation of proteins modified by  
 CC phosphorylation of serine, threonine or tyrosine residues. The  
 CC phosphatases are useful for treating a variety of diseases: for example  
 CC cancer e.g. breast, urogenital, prostate, head, neck, lung cancers,  
 CC synovial sarcomas, renal cell carcinoma, non-small cell lung cancer,  
 CC hepatocellular carcinoma, pancreatic endocrine tumours, stomach cancer,  
 CC glioblastoma, colorectal cancer and thyroid cancer, pathophysiological  
 CC hypoxia, cardiac dysfunction and/or vascular disorders, myopathies,  
 CC congenital muscle disorders, Papillon-Lefevre syndrome, Cowden disease,  
 CC ectodermal dysplasia, Moebius syndrome, Bjornstad syndrome, Bannayan  
 CC Zonana syndrome, schizophrenia and hamartomas  
 XX  
 SQ Sequence 184 AA;  
 Query Match 100.0%; Score 975; DB 4; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-108;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNGMKNKILPGLYIGNFKDARDAEQLSKNKTHTLSVHDSARPMLGKVKLCIPADSPS 60  
 DB 1 MNGMKNKILPGLYIGNFKDARDAEQLSKNKTHTLSVHDSARPMLGKVKLCIPADSPS 60  
 QY 61 QNLTTRHFKESTKFTHECRLGESCLVHCLAGVRSVTLVIAYIMTVTDFGWEDALHTVRA 120  
 DB 61 QNLTTRHFKESTKFTHECRLGESCLVHCLAGVRSVTLVIAYIMTVTDFGWEDALHTVRA 120  
 QY 121 GRSCANPNVGFQRLQEFKEHVEHQYRWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180  
 DB 121 GRSCANPNVGFQRLQEFKEHVEHQYRWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180  
 QY 181 LRRL 184  
 DB 181 LRRL 184  
 RESULT 3  
 AAB66431  
 ID AAB66431 standard; protein; 184 AA.  
 XX  
 AC AAB66431;  
 XX  
 DT 06-APR-2001 (first entry)  
 XX  
 DE Human DSP-3 protein.  
 XX  
 KW Human; DSP-3; cytostatic; immunosuppressive; antiallergic;  
 KW dual specificity phosphatase-3; cell proliferation; metabolic diseases;  
 KW Duchenne muscular dystrophy; cancer; graft-versus-host disease;  
 KW autoimmune disease; allergy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200102582-A1. NPA  
 XX  
 PD 11-JAN-2001.  
 XX  
 PF 29-JUN-2000; 2000WO-US018207.  
 XX

PR 02-JUL-1999; 99US-0142338P.  
 PR 07-APR-2000; 2000WO-US009185.  
 PR 20-APR-2000; 2000WO-US010868.  
 XX  
 PA (CEPT-) CEPTYR INC.  
 XX  
 PI Luche RM, Wei B;  
 XX  
 DR WPI; 2001-138149/14.  
 DR N-PSDB; AAF29601.  
 XX  
 PT New dual-specificity phosphatase (DSP)-3 and DSP-3 alternate form  
 PT polypeptides, useful for identifying modulators DSP-3 or DSP-3 alternate  
 PT form activity, especially for treating e.g. cancer, autoimmune diseases  
 PT or allergies.  
 XX  
 PS Claim 1; Fig 2; 86pp; English.  
 XX  
 CC The present sequence is given in a specification providing human dual  
 CC specificity phosphatase-3 (DSP-3) and a murine DSP-3 variant polypeptide.  
 CC The polypeptides are useful for dephosphorylating a substrate of DSP-3,  
 CC e.g. MAP-kinase. They may be used to treat or prevent diseases associated  
 CC with cell proliferation, immunosuppression, metabolic diseases, or  
 CC abnormal cell growth or cell cycle abnormalities. They are also useful  
 CC for identifying agents that modulate their activity. The modulators are  
 CC useful for treating disorders associated with DSP-3 or DSP-3 variant  
 CC activity, e.g. Duchenne muscular dystrophy, cancer, graft-versus-host  
 CC disease, autoimmune diseases, allergies, metabolic diseases, abnormal  
 CC cell growth, abnormal cell proliferation and cell cycle abnormalities.  
 CC The modulating agents are useful for modulating, modifying or altering  
 CC cellular responses, e.g. in vivo or in vitro cell proliferation,  
 CC differentiation or survival  
 XX  
 SQ Sequence 184 AA;  
 Query Match 100.0%; Score 975; DB 4; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-108;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNGMKNKILPGLYIGNFKDARDAEQLSKNVTHILSVHDSARPMLGKVKYLCIPAAADSPS 60  
 DB 1 MNGMKNKILPGLYIGNFKDARDAEQLSKNVTHILSVHDSARPMLGKVKYLCIPAAADSPS 60  
 QY 61 QNLTFRHFKESIKFTHCRLRGESCLVHCLAGVSRVTLVIAYINTVDFGWEDALHTVRA 120  
 DB 61 QNLTFRHFKESIKFTHCRLRGESCLVHCLAGVSRVTLVIAYINTVDFGWEDALHTVRA 120  
 QY 121 GRSCANPNVGFQRLQEFKEHVEHQYQWLKEEYGESPLQDAEAKNILAAPGILKFWAF 180  
 DB 121 GRSCANPNVGFQRLQEFKEHVEHQYQWLKEEYGESPLQDAEAKNILAAPGILKFWAF 180  
 QY 181 LRLR 184  
 DB 181 LRLR 184  
 RESULT 4  
 AAG78217  
 ID AAG78217 standard; protein; 184 AA.  
 XX  
 AC AAG78217;  
 XX  
 DT 13-DEC-2001 (first entry)  
 XX  
 DE Human MAP kinase interacting kinase phosphatase x.  
 XX  
 KW Human; MAP kinase interacting kinase phosphatase x; hMKPx; adrenal gland.  
 XX  
 OS Homo sapiens.  
 XX  
 FN CN1301869-A.  
 XX  
 PD 04-JUL-2001.

NPA

XX 27-DEC-1999; 99CN-00125397.  
 XX 27-DEC-1999; 99CN-00125397.  
 PR  
 PA (SREH-) SOUTHERN RES CENT STATE HUMAN GENE GROUP.  
 XX  
 PI Gu J, Peng Y, Li Y;  
 XX  
 DR WPI; 2001-550488/62.  
 DR N-PSDB; AAI64795.  
 XX  
 PT New human mitogen activated protein kinase phosphatase and its code  
 PT sequence.  
 XX  
 PS Claim 4; Fig 2; 25pp; Chinese.  
 XX  
 CC The invention relates to human MAP kinase-interacting kinase phosphatase  
 CC x (Genbank Accession Number AF165519), shortly named hMKPx, expressed in  
 CC adrenal gland tissue of normal human body and its coding sequence as well  
 CC as the preparation and application of the protein and nucleic acid  
 CC sequence and the method of detecting hMKPx nucleic acid sequence and  
 CC polypeptide in sample  
 XX  
 SQ Sequence 184 AA;  
 Query Match 100.0%; Score 975; DB 4; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-108;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNGMKNKILPGLYIGNFKDARDAEQLSKNVTHILSVHDSARPMLGKVKYLCIPAAADSPS 60  
 DB 1 MNGMKNKILPGLYIGNFKDARDAEQLSKNVTHILSVHDSARPMLGKVKYLCIPAAADSPS 60  
 QY 61 QNLTFRHFKESIKFTHCRLRGESCLVHCLAGVSRVTLVIAYINTVDFGWEDALHTVRA 120  
 DB 61 QNLTFRHFKESIKFTHCRLRGESCLVHCLAGVSRVTLVIAYINTVDFGWEDALHTVRA 120  
 QY 121 GRSCANPNVGFQRLQEFKEHVEHQYQWLKEEYGESPLQDAEAKNILAAPGILKFWAF 180  
 DB 121 GRSCANPNVGFQRLQEFKEHVEHQYQWLKEEYGESPLQDAEAKNILAAPGILKFWAF 180  
 QY 181 LRLR 184  
 DB 181 LRLR 184  
 RESULT 5  
 AAB67167  
 ID AAB67167 standard; protein; 184 AA.  
 XX  
 AC AAB67167;  
 XX  
 DT 12-APR-2001 (first entry)  
 XX  
 DE Human dual-specificity phosphatase DSP-3.  
 XX  
 KW Human; DSP-3; dual-specificity phosphatase; cell proliferation;  
 KW cell signalling; cancer; graft-versus-host disease; autoimmune disease;  
 KW allergy; metabolic disease; Duchenne muscular dystrophy.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200102581-A1.  
 XX  
 PD 11-JAN-2001.  
 XX  
 PF 20-APR-2000; 2000WO-US010868.  
 XX  
 PR 02-JUL-1999; 99US-0142338P.  
 PR 07-APR-2000; 2000WO-US009185.  
 XX  
 PA (CEPT-) CEPTYR INC.

NPA



XX Luche RM, Wei B;  
XX WPI; 2001-138148/14.  
DR N-PSDB; AAF32191.  
XX  
PT New dual-specificity phosphatase-3 polypeptide and its variants useful  
PT for treating disorders associated with DSP-3 activity, defects in cell  
PT proliferation, differentiation or survival, e.g. Duchenne muscular  
PT dystrophy, cancer.  
XX  
PS Claim 1; Fig 2; 70pp; English.  
XX  
CC The present invention provides the protein and coding sequences of the  
CC human dual-specificity phosphatase DSP-3. The DSP-3 protein is involved  
CC in cell signalling and the sequences can be used in the treatment of  
CC cancer, metabolic and autoimmune diseases, allergies, graft-versus-host  
CC disease, abnormal cell proliferation and Duchenne muscular dystrophy  
XX  
SQ Sequence 184 AA;  
Query Match 100.0%; Score 975; DB 4; Length 184;  
Best Local Similarity 100.0%; Pred. No. 3.2e-108;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNGMKNKILPGLYIGNFKDARDAEQLSKNKVTHLSVHDSARPMLGKVKYLCIPADSPS 60  
DB 1 MNGMKNKILPGLYIGNFKDARDAEQLSKNKVTHLSVHDSARPMLGKVKYLCIPADSPS 60  
QY 61 QNLTFRHFKESIKFTHCECLRGESCLVHCLAGVSRVTLVIAYIMTVTDFGWEDALHTVRA 120  
DB 61 QNLTFRHFKESIKFTHCECLRGESCLVHCLAGVSRVTLVIAYIMTVTDFGWEDALHTVRA 120  
QY 121 GRSCANPNVGFQRLQEFKEHVEHQYRQWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180  
DB 121 GRSCANPNVGFQRLQEFKEHVEHQYRQWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180  
QY 181 LRRL 184  
DB 181 LRRL 184  
RESULT 6  
ID ABB90435 standard; protein; 184 AA.  
AC ABB90435;  
XX  
DT 24-MAY-2002 (first entry)  
XX  
DE Human polypeptide SEQ ID NO 2811.  
XX  
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; anti-ulcer;  
KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;  
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;  
KW neurological disease; infection; human; secreted protein.  
XX  
OS Homo sapiens.  
XX  
PN WO200190304-A2.  
XX  
XX 29-NOV-2001.  
PD  
XX 18-MAY-2001; 2001WO-US016450.  
PF  
XX 19-MAY-2000; 2000US-0205515P.  
PR  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA  
XX Birse CE, Rosen CA;  
FI  
XX WPI; 2002-122018/16.  
DR

DR N-PSDB; ABL90844.  
XX  
PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and  
PT prevention of neural, immune system, muscular, reproductive,  
PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative  
PT disorders.  
XX  
XX Claim 11; SEQ ID NO 2811; 2081pp + Sequence Listing; English.  
PS  
XX The invention relates to novel genes (ABL9449-ABL90853) and proteins  
CC (ABB9040-ABB90444) useful for preventing, treating or ameliorating  
CC medical conditions e.g. by protein or gene therapy. The genes are  
CC isolated from a range of human tissues disclosed in the specification.  
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in  
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and  
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,  
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune  
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic  
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,  
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)  
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing  
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)  
CC infectious diseases such as viral, bacterial, fungal and parasitic  
CC infections. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 184 AA;  
Query Match 100.0%; Score 975; DB 5; Length 184;  
Best Local Similarity 100.0%; Pred. No. 3.2e-108;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNGMKNKILPGLYIGNFKDARDAEQLSKNKVTHLSVHDSARPMLGKVKYLCIPADSPS 60  
DB 1 MNGMKNKILPGLYIGNFKDARDAEQLSKNKVTHLSVHDSARPMLGKVKYLCIPADSPS 60  
QY 61 QNLTFRHFKESIKFTHCECLRGESCLVHCLAGVSRVTLVIAYIMTVTDFGWEDALHTVRA 120  
DB 61 QNLTFRHFKESIKFTHCECLRGESCLVHCLAGVSRVTLVIAYIMTVTDFGWEDALHTVRA 120  
QY 121 GRSCANPNVGFQRLQEFKEHVEHQYRQWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180  
DB 121 GRSCANPNVGFQRLQEFKEHVEHQYRQWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180  
QY 181 LRRL 184  
DB 181 LRRL 184  
RESULT 7  
AD116892  
ID AD116892 standard; protein; 184 AA.  
XX  
XX AD116892;  
AC  
XX 15-APR-2004 (first entry)  
DT  
XX Human NOVX protein homologue SeqID 428.  
DE  
XX human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;  
KW inflammation; autoimmune disorder; allergy; blood disorder;  
KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;  
KW immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;  
KW Alzheimer's disease; infection; str.  
XX  
OS Homo sapiens.  
XX  
XX WO200268649-A2. NPA  
XX  
XX 06-SEP-2002.  
XX  
XX 31-JAN-2002; 2002WO-US002785.  
PF

XX 31-JAN-2001; 2001US-0265395P.  
 PR 31-JAN-2001; 2001US-0265412P.  
 PR 31-JAN-2001; 2001US-0265514P.  
 PR 31-JAN-2001; 2001US-0265517P.  
 PR 02-FEB-2001; 2001US-0266408P.  
 PR 05-FEB-2001; 2001US-0266767P.  
 PR 07-FEB-2001; 2001US-0266975P.  
 PR 08-FEB-2001; 2001US-0267057P.  
 PR 09-FEB-2001; 2001US-0267459P.  
 PR 15-FEB-2001; 2001US-0267823P.  
 PR 26-FEB-2001; 2001US-0268974P.  
 PR 26-FEB-2001; 2001US-0271664P.  
 PR 27-FEB-2001; 2001US-0271833P.  
 PR 27-FEB-2001; 2001US-0271855P.  
 PR 02-MAR-2001; 2001US-0272788P.  
 PR 02-MAR-2001; 2001US-0273048P.  
 PR 14-MAR-2001; 2001US-0275923P.  
 PR 14-MAR-2001; 2001US-0275947P.  
 PR 14-MAR-2001; 2001US-0275950P.  
 PR 14-MAR-2001; 2001US-0275989P.  
 PR 15-MAR-2001; 2001US-0276448P.  
 PR 15-MAR-2001; 2001US-0276450P.  
 PR 16-MAR-2001; 2001US-0276397P.  
 PR 16-MAR-2001; 2001US-0276768P.  
 PR 20-MAR-2001; 2001US-0278652P.  
 PR 26-MAR-2001; 2001US-0278755P.  
 PR 26-MAR-2001; 2001US-0278778P.  
 PR 29-MAR-2001; 2001US-0279882P.  
 PR 29-MAR-2001; 2001US-0279884P.  
 PR 30-MAR-2001; 2001US-0280147P.  
 PR 11-APR-2001; 2001US-0282922P.  
 PR 11-APR-2001; 2001US-0283083P.  
 PR 20-APR-2001; 2001US-0285133P.  
 PR 23-APR-2001; 2001US-0285749P.  
 PR 03-MAY-2001; 2001US-0288327P.  
 PR 03-MAY-2001; 2001US-0288504P.  
 PR 29-MAY-2001; 2001US-0294047P.  
 PR 30-MAY-2001; 2001US-0294473P.  
 PR 08-JUN-2001; 2001US-0296964P.  
 PR 18-JUN-2001; 2001US-0298959P.  
 PR 19-JUN-2001; 2001US-0299324P.  
 PR 13-AUG-2001; 2001US-0312020P.  
 PR 16-AUG-2001; 2001US-0312889P.  
 PR 16-AUG-2001; 2001US-0312908P.  
 PR 21-AUG-2001; 2001US-0313390P.  
 PR 28-AUG-2001; 2001US-0315470P.  
 PR 31-AUG-2001; 2001US-0316447P.  
 PR 07-SEP-2001; 2001US-0318115P.  
 PR 07-SEP-2001; 2001US-0318118P.  
 PR 12-SEP-2001; 2001US-0318740P.  
 PR 19-SEP-2001; 2001US-0323379P.  
 PR 18-OCT-2001; 2001US-0330245P.  
 PR 18-OCT-2001; 2001US-0330308P.  
 PR 14-NOV-2001; 2001US-0332701P.  
 (CURA-) CURAGEN CORP.  
 Tchernev VT, Spytek KA, Zerhusen BD, Patturajan M, Shinkets RA;  
 Li L, Gangolli EA, Padigara DW, Rastelli L, Miller CE;  
 Gerlach VL, Taupier RJ, Gusev VI, Colman SD, Wolenc AR, Pena CE;  
 Furtak K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;  
 WPI; 2002-706998/76.  
 New NOVX polypeptides and nucleic acids, useful for preventing or  
 treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,  
 atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or  
 pharmacogenomics.  
 XX  
 PS Disclosure; SEQ ID NO 428; 1498pp; English.  
 XX  
 CC This invention relates to a novel nucleic acids, and encoded polypeptides

CC thereof, which have properties related to the stimulation of biochemical  
 CC or physiological responses in a cell, tissue, organ or organism.  
 CC Specifically, it refers to the use of biologically active fragments for  
 CC diagnostic and prognostic assays and furthermore in the treatment of  
 CC diverse pathological conditions. The present invention describes novel  
 CC human and murine NOVX proteins, as well as methods to modulate their  
 CC expression using antisense oligos, ribozymes and peptide nucleic acids.  
 CC The NOVX polypeptides, polynucleotides and antibodies are useful in  
 CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,  
 CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in  
 CC treating or preventing diseases such as inflammation, autoimmune  
 CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome  
 CC (AIDS), obesity, asthma, immunoglobulin (IgA) nephropathy, cirrhosis,  
 CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy  
 CC and epilepsy. Accordingly, these molecules have many activities including  
 CC cytosolic, cardiac, antiinflammatory, immunosuppressive, antiallergic,  
 CC haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,  
 CC antiasthmatic, nephrotropic, antiarthritic, hepatotropic,  
 CC neuroprotective, nootropic, antibacterial, virucide, antiparasitic,  
 CC relaxant and anticonvulsant. In addition, they are useful in screening  
 CC assays to identify small molecules that modulate or inhibit, for example,  
 CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also  
 CC used as in chromosome mapping, tissue typing, preventive medicine and  
 CC pharmacogenomics. This polypeptide is a homologue of a human NOVX protein  
 CC of the invention.  
 XX  
 SQ Sequence 184 AA;  
 Query Match 100.0%; Score 975; DB 5; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-108;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGNMKNILPGLYIGNFKDARDARQLSKNKKVTHILSVHDSARPMLEGVKYLCIPADSPS 60  
 DB 1 MGNMKNILPGLYIGNFKDARDARQLSKNKKVTHILSVHDSARPMLEGVKYLCIPADSPS 60  
 QY 61 QNLTFRHFESIKFTHECLRGESCLVHCLAGVSRVTLVIAYIMTVDFGWEDALHTVRA 120  
 DB 61 QNLTFRHFESIKFTHECLRGESCLVHCLAGVSRVTLVIAYIMTVDFGWEDALHTVRA 120  
 QY 121 GRSCANPNVGFQROLQEFKEHVEHQYRQWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180  
 DB 121 GRSCANPNVGFQROLQEFKEHVEHQYRQWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180  
 QY 181 LRRL 184  
 DB 181 LRRL 184  
 RESULT 8  
 ADIL17160  
 ID ADIL17160 standard; protein; 184 AA.  
 XX ADIL17160;  
 XX AC  
 XX DT 15-APR-2004 (first entry)  
 XX DE Human NOVX protein homologue SeqID 696.  
 XX human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;  
 KW inflammation; autoimmune disorder; allergy; blood disorder;  
 KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;  
 KW immunoglobulin (IgA) nephropathy; cirrhosis; arthritis;  
 KW Alzheimer's disease; infection; str.  
 XX Homo sapiens.  
 XX OS  
 XX WO200268649-A2. NPA  
 XX PN  
 XX 06-SEP-2002.  
 XX PD  
 XX 31-JAN-2002; 2002WO-US002785.  
 XX PF  
 XX

PR 31-JAN-2001; 2001US-0265395P.  
PR 31-JAN-2001; 2001US-0265412P.  
PR 31-JAN-2001; 2001US-0265514P.  
PR 31-JAN-2001; 2001US-0265517P.  
PR 05-FEB-2001; 2001US-0266406P.  
PR 05-FEB-2001; 2001US-0266767P.  
PR 07-FEB-2001; 2001US-0266975P.  
PR 07-FEB-2001; 2001US-0270577P.  
PR 08-FEB-2001; 2001US-0267459P.  
PR 09-FEB-2001; 2001US-0267823P.  
PR 15-FEB-2001; 2001US-0268974P.  
PR 26-FEB-2001; 2001US-0271664P.  
PR 27-FEB-2001; 2001US-0271839P.  
PR 27-FEB-2001; 2001US-0271855P.  
PR 02-MAR-2001; 2001US-0272786P.  
PR 02-MAR-2001; 2001US-0273046P.  
PR 14-MAR-2001; 2001US-0275925P.  
PR 14-MAR-2001; 2001US-0275947P.  
PR 14-MAR-2001; 2001US-0275950P.  
PR 14-MAR-2001; 2001US-0275989P.  
PR 15-MAR-2001; 2001US-0276448P.  
PR 15-MAR-2001; 2001US-0276450P.  
PR 16-MAR-2001; 2001US-0276397P.  
PR 16-MAR-2001; 2001US-0276768P.  
PR 20-MAR-2001; 2001US-0278652P.  
PR 26-MAR-2001; 2001US-0278775P.  
PR 26-MAR-2001; 2001US-0278778P.  
PR 29-MAR-2001; 2001US-0279882P.  
PR 29-MAR-2001; 2001US-0279884P.  
PR 30-MAR-2001; 2001US-0280147P.  
PR 11-APR-2001; 2001US-0282992P.  
PR 11-APR-2001; 2001US-0283083P.  
PR 20-APR-2001; 2001US-0285133P.  
PR 23-APR-2001; 2001US-0285749P.  
PR 03-MAY-2001; 2001US-0288327P.  
PR 03-MAY-2001; 2001US-0288504P.  
PR 29-MAY-2001; 2001US-0294047P.  
PR 30-MAY-2001; 2001US-0294473P.  
PR 08-JUN-2001; 2001US-0296964P.  
PR 18-JUN-2001; 2001US-0298959P.  
PR 19-JUN-2001; 2001US-0299324P.  
PR 13-AUG-2001; 2001US-0312020P.  
PR 16-AUG-2001; 2001US-0312889P.  
PR 16-AUG-2001; 2001US-0312908P.  
PR 21-AUG-2001; 2001US-0313390P.  
PR 28-AUG-2001; 2001US-0315470P.  
PR 31-AUG-2001; 2001US-0316447P.  
PR 07-SEP-2001; 2001US-0318115P.  
PR 07-SEP-2001; 2001US-0318118P.  
PR 12-SEP-2001; 2001US-0318740P.  
PR 19-SEP-2001; 2001US-0323379P.  
PR 18-OCT-2001; 2001US-0330245P.  
PR 18-OCT-2001; 2001US-0330308P.  
PR 14-NOV-2001; 2001US-0332701P.  
PA (CURA-) CURAGEN CORP.  
XX Tchernev VT, Spytek KA, Zerhusen BD, Patturajan M, Shinkets RA;  
XX Li L, Gangolli EA, Padigaru DW, Rastelli L, Miller CE;  
PI Gerlach VL, Taupier RJ, Gusev VV, Colman SD, Wolenc AR, Pena CE;  
PI Furtak K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;  
XX WPI; 2002-706998/76.  
DR  
XX  
XX New NOVX polypeptides and nucleic acids, useful for preventing or  
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,  
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or  
PT pharmacogenomics.  
XX  
XX  
PS Disclosure; SEQ ID NO 696; 1498pp; English.  
XX  
XX This invention relates to a novel nucleic acids, and encoded polypeptides  
XX thereof, which have properties related to the stimulation of biochemical

CC or physiological responses in a cell, tissue, organ or organism.  
CC Specifically, it refers to the use of biologically active fragments for  
CC diagnostic and prognostic assays and furthermore in the treatment of  
CC diverse pathological conditions. The present invention describes novel  
CC human and murine NOVX proteins, as well as methods to modulate their  
CC expression using antisense oligos, ribozymes and peptide nucleic acids.  
CC The NOVX polypeptides, polynucleotides and antibodies are useful in  
CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,  
CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in  
CC treating or preventing diseases such as inflammation, autoimmune  
CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome  
CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,  
CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy  
CC and epilepsy. Accordingly, these molecules have many activities including  
CC cytoskeletal, cardiac, anti-inflammatory, immunosuppressive, antiallergic,  
CC haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,  
CC neuroprotective, neurotropic, antibacterial, virucide, hepatotropic,  
CC antiasthmatic, nephrotropic, antitubercular, antiparasitic,  
CC relaxant and anticonvulsant. In addition, they are useful in screening  
CC assays to identify small molecules that modulate or inhibit, for example,  
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also  
CC used as in chromosome mapping, tissue typing, preventive medicine and  
CC pharmacogenomics. This polypeptide is a homologue of a human NOVX protein  
CC of the invention.  
XX  
SQ Sequence 184 AA;

Query Match 100.0%; Score 975; DB 5; Length 184;  
Best Local Similarity 100.0%; Pred. No. 3.2e-108;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGNMKNILPGLYIGNFKDARDAEQLSKNVTHTLSVHDSARPMLEGVKYLICIPAADS 60  
Db 1 MGNMKNILPGLYIGNFKDARDAEQLSKNVTHTLSVHDSARPMLEGVKYLICIPAADS 60  
Qy 61 QNLTTRHFKESIKFTHECLRGESCLVHCLAGVSRSVTLVIAYIMTVDFGWEDALHTVRA 120  
Db 61 QNLTTRHFKESIKFTHECLRGESCLVHCLAGVSRSVTLVIAYIMTVDFGWEDALHTVRA 120  
Qy 121 GRSCANPNVGFQRLQEFKEHVEHQVQLKEEYGESPLQDAEAKNLAAPGILKFWAF 180  
Db 121 GRSCANPNVGFQRLQEFKEHVEHQVQLKEEYGESPLQDAEAKNLAAPGILKFWAF 180  
Qy 181 LRRL 184  
Db 181 LRRL 184

## RESULT 9

ABR42923  
ID ABR42923 standard; protein; 184 AA.

XX ABR42923;

XX 08-SEP-2003 (first entry)

XX Human mitogen-activated protein kinase phosphatase X (MKPX).

XX Mitogen-activated protein kinase phosphatase X; MKPX; enzyme; human;  
XX cancer; vaccine; gene therapy; cytostatic.

XX Homo sapiens.

XX WO2003044161-A2.

XX 30-MAY-2003.

XX 05-NOV-2002; 2002WO-US035312.

XX 15-NOV-2001; 2001US-0331394P.

XX (TULA-) TULARIK INC.

NPA

PI Sin WC, Yang J;  
 DR WPI; 2003-457600/43.  
 DR N-PSDB; ACC83479.  
 XX  
 PT New isolated mitogen-activated protein kinase phosphatase X gene  
 PT amplicon, useful for diagnosing, preventing and treating pre-cancerous  
 PT lesions or cancer in a mammal, e.g. colon, prostate or ovarian cancer.  
 PS  
 PS Claim 12; Page 90; 90pp; English.  
 XX  
 CC The present sequence is the protein sequence of human mitogen-activated  
 CC protein kinase phosphatase X (MKPX). MKPX is amplified and overexpressed  
 CC in human cancers, including colon cancer, ovarian cancer and prostate  
 CC cancer. The MKPX gene, its expressed protein products and antibodies can  
 CC be used diagnostically or as targets for cancer therapy or vaccine. They  
 CC are also used to identify compounds and reagents useful in cancer  
 CC diagnosis, prevention and therapy, and for determining the efficacy of a  
 CC therapeutic treatment regimen in a patient. A claimed method of blocking  
 CC in vivo expression of the gene involves administering a vector encoding  
 CC MKPX small interfering RNA (siRNA).  
 XX  
 XX Sequence 184 AA;  
 SQ  
 Query Match 100.0%; Score 975; DB 6; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-108;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGNQMKILPGLYIGNFKDARDAEQLSKNKHVTHLSVHDSARPMLGKYLICIPAADS 60  
 DB 1 MGNQMKILPGLYIGNFKDARDAEQLSKNKHVTHLSVHDSARPMLGKYLICIPAADS 60  
 QY 61 QNLTTHPKESIKFTHECLRGESCLVHCLAGVSRVTLVIAYIMTVDFGWEDALHTVRA 120  
 DB 61 QNLTTHPKESIKFTHECLRGESCLVHCLAGVSRVTLVIAYIMTVDFGWEDALHTVRA 120  
 QY 121 GRSCANPNVGFQRLQEFKEHVEHQYRWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180  
 DB 121 GRSCANPNVGFQRLQEFKEHVEHQYRWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180  
 QY 181 LRRL 184  
 DB 181 LRRL 184  
 RESULT 10  
 ADD89787  
 ID ADD89787 standard; protein; 184 AA.  
 XX  
 AC ADD89787;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human MKPX protein SEQ ID NO:2.  
 XX  
 KW cancer associated phosphatase; enzyme; human; cancer; tumour; cytostatic;  
 KW immunosuppressive; antidiabetic; neuroprotective; antirheumatic;  
 KW antiarthritic; antipariatic; antiarteriosclerotic; antiinflammatory;  
 KW vulnary; gynaecological; angiogenic; hyperproliferative disease;  
 KW autoimmune disease; diabetes mellitus; multiple sclerosis;  
 KW rheumatoid arthritis; psoriasis; atherosclerosis; inflammation; scarring;  
 KW endometriosis; angiogenesis.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO2003083102-A2.  
 XX  
 PD 09-OCT-2003.  
 XX  
 PF 19-MAR-2003; 2003WO-CA000393.  
 XX  
 PR 28-MAR-2002; 2002US-0368859P.  
 XX

PA (KINE-) KINETEK PHARM INC.  
 PI Delaney AD;  
 XX  
 DR WPI; 2003-902934/82.  
 DR N-PSDB; ADD89786.  
 XX  
 PT New nucleic acids encoding cancer associated phosphatases, useful as  
 PT targets for screening pharmaceutical agents that inhibit the growth of  
 PT tumor cells, or for diagnosing and treating cancer, inflammation or  
 PT autoimmune disease.  
 XX  
 XX Claim 1; SEQ ID NO 2; 63pp; English.  
 PS  
 XX The present invention describes an isolated cancer associated phosphatase  
 CC nucleic acid. Also described: (1) a method of screening for biologically  
 CC active agents that modulate a cancer associated phosphatase function; (2)  
 CC a method for the diagnosis of cancer; (3) a method for inhibiting the  
 CC growth of a cancer cell; (4) methods of screening for targets of a cancer  
 CC associated phosphatase, where the targets are associated with signal  
 CC transduction in cancer cells; (5) a compound (C) for the treatment of a  
 CC tumour; (6) a composition for the treatment of a tumour comprising a  
 CC pharmaceutical carrier and (C); (7) methods for treating a tumour; and  
 CC (8) a method for visualising a tumour in a patient. A cancer associated  
 CC phosphatase of the present invention has cytostatic, immunosuppressive,  
 CC antidiabetic, neuroprotective, antirheumatic, antiarthritic,  
 CC antipariatic, antiarteriosclerotic, antiinflammatory, vulnary,  
 CC gynaecological and angiogenic activities. The cancer associated  
 CC phosphatases and nucleic acids encoding the proteins are useful for  
 CC visualising tumours in patients or diagnosing and treating cancer, e.g.  
 CC pancreas, lung, ovarian, liver or colon cancer. The polypeptides and  
 CC nucleic acids may also be used for treating hyperproliferative diseases,  
 CC such as autoimmune disease, diabetes mellitus, multiple sclerosis,  
 CC rheumatoid arthritis, psoriasis, atherosclerosis, inflammation, scarring,  
 CC endometriosis or angiogenesis, determining the effectiveness of drugs,  
 CC determining patient prognosis, or as targets for screening pharmaceutical  
 CC agents that inhibit the growth or metastasis of tumour cells. The present  
 CC sequence represents the human cancer associated phosphatase MKPX, which  
 CC is used in the exemplification of the present invention.  
 XX  
 SQ Sequence 184 AA;  
 Query Match 100.0%; Score 975; DB 7; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-108;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGNQMKILPGLYIGNFKDARDAEQLSKNKHVTHLSVHDSARPMLGKYLICIPAADS 60  
 DB 1 MGNQMKILPGLYIGNFKDARDAEQLSKNKHVTHLSVHDSARPMLGKYLICIPAADS 60  
 QY 61 QNLTTHPKESIKFTHECLRGESCLVHCLAGVSRVTLVIAYIMTVDFGWEDALHTVRA 120  
 DB 61 QNLTTHPKESIKFTHECLRGESCLVHCLAGVSRVTLVIAYIMTVDFGWEDALHTVRA 120  
 QY 121 GRSCANPNVGFQRLQEFKEHVEHQYRWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180  
 DB 121 GRSCANPNVGFQRLQEFKEHVEHQYRWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180  
 QY 181 LRRL 184  
 DB 181 LRRL 184  
 RESULT 11  
 ADD89787  
 ID ADD89787 standard; protein; 184 AA.  
 XX  
 AC ADD89787;  
 XX  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Human signal transduction-associated protein SEQ ID 779.  
 XX

KW small interfering RNA; siRNA; protein-tyrosine-phosphatase; PTP;  
 KW cytosolic; immunomodulator; antimicrobial; antiinflammatory;  
 KW antidiabetic; anorectic; cancer; autoimmune disease; infection;  
 KW inflammation; diabetes; obesity; RNA interference; gene silencing.  
 XX Homo sapiens.  
 XX WO2004016735-A2. **NPA**  
 XX 26-FEB-2004.  
 XX 23-MAY-2003; 2003WO-US016632.  
 XX 23-MAY-2002; 2002US-0383249P.  
 XX 14-APR-2003; 2003US-0462942P.  
 XX (CEPT-) CEPTVR INC.  
 XX (COLD-) COLD SPRING HARBOR LAB.  
 XX Klinghoffer R, Lewis SP, Tonks NK, Meng T;  
 XX WPI; 2004-203773/39.  
 XX N-PSDB; ADN75953.  
 XX New isolated small interfering RNA (siRNA) polynucleotide useful for  
 PT treating diseases with aberrant activity of the protein tyrosine  
 PT phosphatase, such as cancer, autoimmune disease, infection, inflammation,  
 PT diabetes and obesity.  
 XX Disclosure; SEQ ID NO 779; 392pp; English.  
 XX This invention describes novel small interfering RNA (siRNA)  
 CC polynucleotides capable of interfering with expression of a polypeptide  
 CC having protein-tyrosine-phosphatase (PTP) activity. The products of the  
 CC invention have cytostatic, immunomodulator, antimicrobial,  
 CC antiinflammatory, antidiabetic and anorectic activity. The methods and  
 CC compositions of the present invention are useful for treating diseases or  
 CC conditions associated with aberrant expression or activity of the protein  
 CC tyrosine phosphatase, such as cancer, autoimmune diseases, infection,  
 CC inflammation, diabetes and obesity. This sequence represents a siRNA  
 CC directed against dual specificity phosphatase (DSP) expression.  
 XX SQ Sequence 184 AA;  
 Query Match 100.0%; Score 975; DB 8; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-108;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGNMKNILPGLYIGNFKDARDQSLSKNVTHILSVHDSARPMLGVKYLICIPADSPS 60  
 Db 1 MGNMKNILPGLYIGNFKDARDQSLSKNVTHILSVHDSARPMLGVKYLICIPADSPS 60  
 QY 61 QNLTTRHFKESIKFIEHCELRGESCLVHCLAGVSRSVTLVIAYIMTVDFGWEDALHTVRA 120  
 Db 61 QNLTTRHFKESIKFIEHCELRGESCLVHCLAGVSRSVTLVIAYIMTVDFGWEDALHTVRA 120  
 QY 121 GRSCANPNVGFQRLQEPKEHVEHQYRWLKEEYGESPLQDAEAKNIIAAPGILKFWAF 180  
 Db 121 GRSCANPNVGFQRLQEPKEHVEHQYRWLKEEYGESPLQDAEAKNIIAAPGILKFWAF 180  
 QY 181 LRRLL 184  
 Db 181 LRRLL 184  
 RESULT 12  
 ADP25001  
 ID ADP25001 standard; protein; 184 AA.  
 XX  
 AC ADP25001;  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX

DE PRO polypeptide SEQ ID NO:2179.  
 XX PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;  
 KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;  
 KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.  
 XX Unidentified.  
 XX WO2004041170-A2. **NPA**  
 XX 21-MAY-2004.  
 XX 30-OCT-2003; 2003WO-US034312.  
 XX 01-NOV-2002; 2002US-0423394P.  
 XX (GETH ) GENENTECH INC.  
 XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WT;  
 PI Wu TD;  
 PI WPI; 2004-419628/39.  
 DR N-PSDB; ADP25000.  
 XX New PRO polypeptides and polynucleotides, useful for treating e.g.  
 PT erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated  
 PT renal disease, or demyelinating diseases of the central or peripheral  
 PT nervous system.  
 XX Claim 7; SEQ ID NO 2179; 2940pp; English.  
 XX The invention relates to a novel isolated nucleic acid and the PRO  
 CC polypeptide encoded by it. A protein of the invention has  
 CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,  
 CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,  
 CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide  
 CC of the invention may have a use in gene therapy. The PRO polypeptide, its  
 CC agonist, antagonist, or antibody that specifically binds to the  
 CC polypeptide is useful for treating an immune related disorder such as  
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an  
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal  
 CC disease, a demyelinating disease of the central or peripheral nervous  
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,  
 CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary  
 CC disease, infectious or autoimmune chronic active hepatitis, primary  
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,  
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's  
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin  
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic  
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food  
 CC hypersensitivity, urticaria, an immunologic disease of the lung,  
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity  
 CC pneumonitis, a transplantation associated disease, graft rejection or  
 CC graft-versus-host disease. The present sequence represents a PRO protein  
 CC of the invention.  
 XX SQ Sequence 184 AA;  
 Query Match 100.0%; Score 975; DB 8; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-108;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGNMKNILPGLYIGNFKDARDQSLSKNVTHILSVHDSARPMLGVKYLICIPADSPS 60  
 Db 1 MGNMKNILPGLYIGNFKDARDQSLSKNVTHILSVHDSARPMLGVKYLICIPADSPS 60  
 QY 61 QNLTTRHFKESIKFIEHCELRGESCLVHCLAGVSRSVTLVIAYIMTVDFGWEDALHTVRA 120  
 Db 61 QNLTTRHFKESIKFIEHCELRGESCLVHCLAGVSRSVTLVIAYIMTVDFGWEDALHTVRA 120

QY 121 GRSCANPVGFQRLQEFKEKHEVHOYRWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180  
Db 121 GRSCANPVGFQRLQEFKEKHEVHOYRWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180  
QY 181 LRRLL 184  
Db 181 LRRLL 184

RESULT 13  
AAU23521  
ID AAU23521 standard; protein; 190 AA.  
XX  
AC AAU23521;  
XX  
DT 17-DEC-2001 (first entry)  
XX  
DE Novel human enzyme polypeptide #607.  
XX  
KW Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;  
KW ligase; hyperproliferative disorder; immunodeficiency disorder;  
KW autoimmune disorder; neurological disorder; metabolic disorder;  
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;  
KW blood-related disorder; infectious disorder; cytostatic; anti arthritic;  
KW nephrotropic; anticoagulant.  
XX  
OS Homo sapiens.  
XX  
XX  
PN WO200155301-A2.  
XX  
PD 02-AUG-2001.  
XX  
XX 17-JAN-2001; 2001WO-US001239.  
XX  
PR 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
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PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225266P.  
PR 14-AUG-2000; 2000US-0225267P.  
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PR 14-AUG-2000; 2000US-0225270P.  
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PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
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PR 18-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226868P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
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PR 06-SEP-2000; 2000US-0230437P.  
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PR 08-SEP-2000; 2000US-0231242P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
PR 08-SEP-2000; 2000US-0231413P.  
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PR 08-SEP-2000; 2000US-0232080P.  
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PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
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PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0233063P.  
PR 14-SEP-2000; 2000US-0233064P.  
PR 14-SEP-2000; 2000US-0233065P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234224P.  
PR 25-SEP-2000; 2000US-0234997P.  
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PR 26-SEP-2000; 2000US-0235844P.  
PR 27-SEP-2000; 2000US-0235836P.  
PR 27-SEP-2000; 2000US-0235837P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
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PR 02-OCT-2000; 2000US-0237038P.  
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PR 02-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239935P.  
PR 13-OCT-2000; 2000US-0239937P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241221P.  
PR 20-OCT-2000; 2000US-0241785P.  
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PR 20-OCT-2000; 2000US-0241787P.  
PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246478P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0246524P.  
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PR 08-NOV-2000; 2000US-0246526P.  
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PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 17-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
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PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.

PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249264P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 17-NOV-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 05-DEC-2000; 2000US-0256719P.  
PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
PR 08-DEC-2000; 2000US-0251989P.  
PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Barash SC, Ruben SM;  
XX  
XX WPI; 2001-465566/50.  
DR N-PSDB; AAS41391.  
XX  
PT Novel polypeptides and polynucleotides useful for diagnosing, preventing,  
PT treating neural, immune system, muscular, reproductive, pulmonary,  
PT cardiovascular, renal, proliferative disorders and cancerous diseases.  
XX  
PS Claim 11; SEQ ID NO 1517; 1180pp; English.  
XX  
CC The present invention relates to the isolation of novel human enzyme  
CC polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences  
CC encoding them. The enzyme polypeptides of the invention may comprise the  
CC functional classes of oxidoreductases, transferases, hydrolases, lyases,  
CC isomerases or ligases. The sequences of the invention are useful in the  
CC diagnosis, treatment, prevention and/or prognosis of a wide range of  
CC disorders including hyperproliferative disorders (e.g. cancer),  
CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g.  
CC arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic  
CC disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma),  
CC cardiovascular disorders (e.g. atherosclerosis), blood-related disorders  
CC (e.g. haemophilia), reproductive disorders (e.g. infertility) and  
CC infectious disorders (e.g. influenza). The polynucleotides of the  
CC invention can also be used in gene therapy. AAU22915-AAU23814 represent  
CC the novel human enzyme polypeptides of the invention. Note: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 190 AA;  
Query Match 100.0%; Score 975; DB 4; Length 190;  
Best Local Similarity 100.0%; Pred. No. 3,4e-108; Mismatches 0; Gaps 0;  
Matches 184; Conservative 0; Indels 0; Gaps 0;  
QY 1 MNGNGMKLPLGLYIGNFKDARDAEQLSKNVTHLSVHDSARPMLEGVKYLICIPAADSPS 60  
DB 7 MNGNGMKLPLGLYIGNFKDARDAEQLSKNVTHLSVHDSARPMLEGVKYLICIPAADSPS 66  
QY 61 QNLTRHFESIKFIECELRGESCLVHCLAGVSRVTLVIAYIMTVTDGHEDALHTVRA 120  
DB 67 QNLTRHFESIKFIECELRGESCLVHCLAGVSRVTLVIAYIMTVTDGHEDALHTVRA 126  
QY 121 GRSCANPNVGFQRLQEFEXHEVHOYRWLKEBYGESPLQDAEAKNLAAPGILKFWAF 180  
DB 121 GRSCANPNVGFQRLQEFEXHEVHOYRWLKEBYGESPLQDAEAKNLAAPGILKFWAF 186

Db 127 GRSCANPNVGFQRLQEFEXHEVHOYRWLKEBYGESPLQDAEAKNLAAPGILKFWAF 186  
QY 181 LRRL 184  
DB 187 LRRL 190  
RESULT 14  
AAU21668  
ID AAU21668 standard; protein; 190 AA.  
XX  
AC AAU21668;  
XX  
DT 04-DEC-2001 (first entry)  
XX  
DE Novel human neoplastic disease associated polypeptide #101.  
XX  
KW Human; neoplastic disease associated polypeptide; cancer;  
KW hyperproliferative disorder; neural disorder; immune system disorder;  
KW muscular disorder; reproductive disorder; gastrointestinal disorder;  
KW pulmonary disorder; cardiovascular disorder; renal disorder;  
KW neuroprotective; cytostatic; anti inflammatory; vasotropic.  
XX  
OS Homo sapiens.  
XX  
EN WO200155163-A1.  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US001358.  
XX  
PR 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180828P.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
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PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
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PR 18-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226686P.  
PR 23-AUG-2000; 2000US-0227182P.  
PR 30-AUG-2000; 2000US-0227009P.  
PR 01-SEP-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.





Db 187 LRRL 190

RESULT 15  
AAU21796  
ID AAU21796 standard; protein; 190 AA.  
XX AC AAU21796;  
XX DT 04-DEC-2001 (first entry)  
XX DE Novel human neoplastic disease associated polypeptide #229.  
XX KW Human; neoplastic disease associated polypeptide; cancer;  
KW hyperproliferative disorder; neural disorder; immune system disorder;  
KW muscular disorder; reproductive disorder; gastrointestinal disorder;  
KW pulmonary disorder; cardiovascular disorder; renal disorder;  
KW neuroprotective; cytostatic; anti inflammatory; vasotropic.  
XX OS Homo sapiens.  
XX FN WO200155163-A1.  
XX PD 02-AUG-2001.  
XX PF 17-JAN-2001; 2001WO-US001358.  
XX PR 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 27-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
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PR 11-JUL-2000; 2000US-0217487P.  
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PR 26-JUL-2000; 2000US-0220963P.  
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PR 14-AUG-2000; 2000US-0224518P.  
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PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226686P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
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PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
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PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
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PR 27-SEP-2000; 2000US-0235834P.  
PR 27-SEP-2000; 2000US-0235836P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
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PR 02-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239035P.  
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PR 20-OCT-2000; 2000US-0240960P.  
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PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241786P.  
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PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 01-NOV-2000; 2000US-0241826P.  
PR 08-NOV-2000; 2000US-0246474P.  
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PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
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PR 17-NOV-2000; 2000US-0249214P.  
PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

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1006.009 Million cell updates/sec

Title: US-10-658-661-2

Perfect score: 975

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Scoring table: BLOSUM62

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Searched: 1736639 seqs, 388188149 residues

Total number of hits satisfying chosen parameters: 1736639

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	975	100.0	184	15	US-10-264-237-2811
3	975	100.0	184	15	US-10-072-012-428
4	975	100.0	184	15	US-10-072-012-696
5	975	100.0	184	15	US-10-444-7958-779
6	975	100.0	190	14	US-10-103-313-195
7	975	100.0	190	14	US-10-103-313-523
8	959	98.4	184	14	US-10-151-320-15
9	932	95.6	184	15	US-10-072-012-429
10	932	95.6	184	15	US-10-072-012-697
11	923	94.7	184	15	US-10-072-012-430

12	923	94.7	184	15	US-10-072-012-698	Sequence 698, App
13	897	86.0	205	17	US-10-803-738-2	Sequence 2, Appli
14	843	92.5	205	17	US-10-803-738-4	Sequence 4, Appli
15	690	70.8	138	17	US-10-803-738-5	Sequence 5, Appli
16	673	69.0	162	15	US-10-104-047-3471	Sequence 3471, Ap
17	528	54.2	235	9	US-09-963-204-2	Sequence 2, Appli
18	528	54.2	235	14	US-10-151-320-14	Sequence 14, Appl
19	528	54.2	235	14	US-10-151-320-32	Sequence 32, Appl
20	528	54.2	235	15	US-10-072-012-426	Sequence 426, App
21	528	54.2	235	15	US-10-072-012-695	Sequence 695, App
22	528	54.2	235	15	US-10-444-7958-783	Sequence 783, App
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24	528	54.2	289	14	US-10-151-320-33	Sequence 33, Appl
25	528	54.2	329	9	US-09-963-204-22	Sequence 22, Appl
26	528	54.2	329	14	US-10-151-320-31	Sequence 31, Appl
27	528	54.2	329	15	US-10-168-506-20	Sequence 20, Appl
28	528	54.2	329	15	US-10-343-357-10	Sequence 10, Appl
29	528	54.2	329	17	US-10-838-181-20	Sequence 20, Appl
30	521	53.4	236	15	US-10-072-012-108	Sequence 108, App
31	483.5	49.6	149	14	US-10-151-320-38	Sequence 38, Appl
32	477	48.9	154	14	US-10-151-320-12	Sequence 12, Appl
33	477	48.9	154	15	US-10-444-7958-841	Sequence 841, App
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35	477	48.9	181	14	US-10-151-320-6	Sequence 6, Appli
36	477	48.9	181	14	US-10-151-320-8	Sequence 8, Appli
37	477	48.9	181	15	US-10-444-7958-831	Sequence 831, App
38	477	48.9	181	15	US-10-444-7958-835	Sequence 835, App
39	477	48.9	181	15	US-10-444-7958-837	Sequence 837, App
40	477	48.9	298	14	US-10-151-320-4	Sequence 4, Appli
41	477	48.9	298	15	US-10-444-7958-833	Sequence 833, App
42	476	48.8	92	16	US-10-425-115-335209	Sequence 335209,
43	474	48.6	243	15	US-10-072-012-427	Sequence 427, App
44	474	48.6	243	15	US-10-072-012-694	Sequence 694, App
45	465	47.7	159	14	US-10-151-320-10	Sequence 10, Appl

#### ALIGNMENTS

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US-10-287-806-2  
; Sequence 2, Application US/10287806  
; Publication No. US20030148341A1  
; GENERAL INFORMATION:  
; APPLICANT: SIN, Wun Chey  
; APPLICANT: YANG, Jianxin  
; TITLE OF INVENTION: Gene Amplification and Overexpression in Cancer  
; FILE REFERENCE: 38002-0038  
; CURRENT APPLICATION NUMBER: US/10/287,806  
; CURRENT FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: US 60/331,394  
; PRIOR FILING DATE: 2001-11-15  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 2  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-287-806-2

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Db 181 LRRL 184

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US-10-264-237-2811  
; Sequence 2811, Application US/10264237  
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; APPLICANT: Birse et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PA131P1  
; CURRENT APPLICATION NUMBER: US/10/264,237  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: PCT/US01/16450  
; PRIOR FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: US 60/205,515  
; PRIOR FILING DATE: 2000-05-19  
; NUMBER OF SEQ ID NOS: 2876  
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; ORGANISM: Homo sapiens  
US-10-264-237-2811

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US-10-072-012-428  
; Sequence 428, Application US/10072012  
; Publication No. US20040033493A1  
; GENERAL INFORMATION:  
; APPLICANT: Tchernev, Velizar  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Zerhusen, Bryan  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Shimkets, Richard  
; APPLICANT: Li, Li  
; APPLICANT: Gangolli, Esha  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Anderson, David W.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Taupier Jr, Raymond J.  
; APPLICANT: Gusev, Vladimir Y.  
; APPLICANT: Colman, Steven D.  
; APPLICANT: Wolenc, Adam R.  
; APPLICANT: Pena, Carol E. A

; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Grosse, William M.  
; APPLICANT: Alsobrook II, John P.  
; APPLICANT: Lepley, Denise M.  
; APPLICANT: Riéger, Daniel K.  
; APPLICANT: Burgess, Catherine E.  
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-258  
; CURRENT APPLICATION NUMBER: US/10/072,012  
; CURRENT FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: 60/265,102  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: 60/265,514  
; PRIOR FILING DATE: 2001-01-31  
; PRIOR APPLICATION NUMBER: 60/265,517  
; PRIOR FILING DATE: 2001-01-31  
; PRIOR APPLICATION NUMBER: 60/265,412  
; PRIOR FILING DATE: 2001-01-31  
; PRIOR APPLICATION NUMBER: 60/265,395  
; PRIOR FILING DATE: 2001-01-31  
; PRIOR APPLICATION NUMBER: 60/266,406  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 60/266,767  
; PRIOR FILING DATE: 2001-02-05  
; PRIOR APPLICATION NUMBER: 60/267,057  
; PRIOR FILING DATE: 2001-02-07  
; PRIOR APPLICATION NUMBER: 60/266,975  
; PRIOR FILING DATE: 2001-02-07  
; PRIOR APPLICATION NUMBER: 60/267,459  
; PRIOR FILING DATE: 2001-02-08  
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; NUMBER OF SEQ ID NOS: 1391  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 428  
; LENGTH: 184  
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; ORGANISM: Homo sapiens  
US-10-072-012-428

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Db 181 LRRL 184

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; Sequence 696, Application US/10072012  
; Publication No. US20040033493A1  
; GENERAL INFORMATION:  
; APPLICANT: Tchernev, Velizar  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Zerhusen, Bryan  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Shimkets, Richard  
; APPLICANT: Li, Li  
; APPLICANT: Gangolli, Esha  
; APPLICANT: Padigaru, Muralidhara

APPLICANT: Anderson, David W.  
APPLICANT: Rastelli, Luca  
APPLICANT: Miller, Charles E.  
APPLICANT: Gerlach, Valerie  
APPLICANT: Taupier Jr, Raymond J.  
APPLICANT: Gusev, Vladimir Y.  
APPLICANT: Coleman, Steven D.  
APPLICANT: Wolenc, Adam R.  
APPLICANT: Futak, Katarzyna  
APPLICANT: Grosse, William M.  
APPLICANT: Alsbrook II, John P.  
APPLICANT: Lepley, Denise M.  
APPLICANT: Rieger, Daniel K.  
APPLICANT: Burgess, Catherine E.  
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
CURRENT APPLICATION NUMBER: US/10/072,012  
CURRENT FILING DATE: 2002-01-31  
PRIOR APPLICATION NUMBER: 60/265,102  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: 60/265,514  
PRIOR FILING DATE: 2001-01-31  
PRIOR APPLICATION NUMBER: 60/265,517  
PRIOR FILING DATE: 2001-01-31  
PRIOR APPLICATION NUMBER: 60/265,412  
PRIOR FILING DATE: 2001-01-31  
PRIOR APPLICATION NUMBER: 60/265,395  
PRIOR FILING DATE: 2001-01-31  
PRIOR APPLICATION NUMBER: 60/266,406  
PRIOR FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: 60/266,767  
PRIOR FILING DATE: 2001-02-05  
PRIOR APPLICATION NUMBER: 60/267,057  
PRIOR FILING DATE: 2001-02-07  
PRIOR APPLICATION NUMBER: 60/266,975  
PRIOR FILING DATE: 2001-02-07  
PRIOR APPLICATION NUMBER: 60/267,459  
PRIOR FILING DATE: 2001-02-08  
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NUMBER OF SEQ ID NOS: 1391  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 696  
LENGTH: 184  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-072-012-696

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Qy 181 LRRL 184  
Db 181 LRRL 184

RESULT 5  
US-10-444-795B-779  
Sequence 779, Application US/10444795B  
Publication No. US20040077574A1

GENERAL INFORMATION:  
APPLICANT: Klinghoffer, Richard  
APPLICANT: Lewis, Stephen Patrick  
TITLE OF INVENTION: MODULATION OF BIOLOGICAL SIGNAL  
TITLE OF INVENTION: TRANSDUCTION BY RNA INTERFERENCE  
FILE REFERENCE: 200125.449  
CURRENT APPLICATION NUMBER: US/10/444,795B  
CURRENT FILING DATE: 2003-05-23  
NUMBER OF SEQ ID NOS: 842  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 779  
LENGTH: 184  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-444-795B-779

Query Match 100.0%; Score 975; DB 15; Length 184;  
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Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MGNMKNILPGLYGNFKDARDAEQLSKNKVTHLSVHDSARPMLGVKYLICIPAADSPS 60  
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Qy 181 LRRL 184  
Db 181 LRRL 184

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US-10-103-313-395  
Sequence 395, Application US/10103313  
Publication No. US20030082758A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: RJ207C1  
CURRENT APPLICATION NUMBER: US/10/103,313  
CURRENT FILING DATE: 2002-03-12  
NUMBER OF SEQ ID NOS: 653  
Prior Application removed - See File Wrapper or Palm  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 395  
LENGTH: 190  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-103-313-395

Query Match 100.0%; Score 975; DB 14; Length 190;  
Best Local Similarity 100.0%; Pred. No. 2.6e-99;  
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Db          187 LRRL 190
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; Publication No. US20030082758A1
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; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: RJZ07C1
; CURRENT APPLICATION NUMBER: US/10/103,313
; CURRENT FILING DATE: 2002-03-12
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; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 523
; LENGTH: 190
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; ORGANISM: Homo sapiens
US-10-103-313-523
Query Match      100.0%; Score 975; DB 14; Length 190;
Best Local Similarity 100.0%; Pred. No. 2.6e-99;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1  MGNMKNILPGLYIGNFKDARDASQLSKNVTILSVHDSARPMLGKYLICIPAAADSPS 60
Db 7  MGNMKNILPGLYIGNFKDARDASQLSKNVTILSVHDSARPMLGKYLICIPAAADSPS 66

Qy 61 QNLTTRHPKESIKFTIHECRLGESCLVHCLAGVSRSVTLVIAYIMTVTDFGWDALHTVRA 120
Db 67 QNLTTRHPKESIKFTIHECRLGESCLVHCLAGVSRSVTLVIAYIMTVTDFGWDALHTVRA 126

Qy 121 GRSCANPNVGFQRLQEFKEHVEHQYRQWLKKEEYGESPLQDAEAKNLAAPGILKFWAF 180
Db 127 GRSCANPNVGFQRLQEFKEHVEHQYRQWLKKEEYGESPLQDAEAKNLAAPGILKFWAF 186

Qy 181 LRRL 184
|||||
RESULT 8
US-10-151-320-15
; Sequence 15, Application US/10151320
; Publication No. US20030092114A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; TITLE OF INVENTION: DSP-18 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.436
; CURRENT APPLICATION NUMBER: US/10/151,320
; CURRENT FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-320-15
Query Match      98.4%; Score 959; DB 14; Length 184;
Best Local Similarity 98.9%; Pred. No. 1.5e-97;
Matches 182; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1  MGNMKNILPGLYIGNFKDARDASQLSKNVTILSVHDSARPMLGKYLICIPAAADSPS 60
Db 1  MGNMKNILPGLYIGNFKDARDASQLSKNVTILSVHDSARPMLGKYLICIPAAADSPS 60

Qy 61 QNLTTRHPKESIKFTIHECRLGESCLVHCLAGVSRSVTLVIAYIMTVTDFGWDALHTVRA 120

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Db          181 LRRL 184
Qy 121 GRSCANPNVGFQRLQEFKEHVEHQYRQWLKKEEYGESPLQDAEAKNLAAPGILKFWAF 180
Db 121 GRSCANPNVGFQRLQEFKEHVEHQYRQWLKKEEYGESPLQDAEAKNLAAPGILKFWAF 180
Qy 181 LRRL 184
Db 181 LRRL 184

RESULT 9
US-10-072-012-429
; Sequence 429, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 429
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-072-012-429
Query Match      95.6%; Score 932; DB 15; Length 184;

```

Best Local Similarity 93.5%; Pred. No. 1.4e-94;  
Matches 172; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGNGMKILPGLYIGNFKDARDAEQLSKNKKVTHLSVHDSARPMLGVKYLICIPAADSPS 60  
Db 1 MGSGMSQLPGLYIGNFKDARDAEQLSKNKKVTHLSVHDTARPMLGVKYLICIPAADTPS 60

Qy 61 QNLTRHPKESIKFTHCRLRGESCLVHCLAGVSRVTLVIAYIMTVDTFGWEDALHTVRA 120  
Db 61 QNLTRHPKESIKFTHCRLRGESCLVHCLAGVSRVTLVIAYIMTVDTFGWEDALHTVRA 120

Qy 121 GRSCANPNVGFQRLQEFKEHVEHGYRQWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180  
Db 121 GRSCANPNLGFQRLQEFKEHVEHGYRQWLKEEYGENPLRDAEAKNLAAPGILKYWAF 180

Qy 181 LRL 184  
Db 181 LRL 184

RESULT 10  
US-10-072-012-697  
; Sequence 697, Application US/10072012  
; Publication No. US20040033493A1  
; GENERAL INFORMATION:  
; APPLICANT: Tchernev, Velizar  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Zerhusen, Bryan  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Shinkets, Richard  
; APPLICANT: Li, Li  
; APPLICANT: Gangolli, Esha  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Anderson, David W.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Taupier Jr, Raymond J.  
; APPLICANT: Gusev, Vladimir Y.  
; APPLICANT: Colman, Steven D.  
; APPLICANT: Wolenc, Adam R.  
; APPLICANT: Pena, Carol E. A  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Grosse, William M.  
; APPLICANT: Alsobrook II, John P.  
; APPLICANT: Lepley, Denise M.  
; APPLICANT: Rieger, Daniel K.  
; APPLICANT: Burgess, Catherine E.  
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-258  
; CURRENT APPLICATION NUMBER: US/10/072,012  
; PRIOR FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: 60/265,102  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: 60/265,514  
; PRIOR FILING DATE: 2001-01-31  
; PRIOR APPLICATION NUMBER: 60/265,517  
; PRIOR FILING DATE: 2001-01-31  
; PRIOR APPLICATION NUMBER: 60/265,412  
; PRIOR FILING DATE: 2001-01-31  
; PRIOR APPLICATION NUMBER: 60/266,767  
; PRIOR FILING DATE: 2001-02-05  
; PRIOR APPLICATION NUMBER: 60/267,057  
; PRIOR FILING DATE: 2001-02-07  
; PRIOR APPLICATION NUMBER: 60/266,975  
; PRIOR FILING DATE: 2001-02-07  
; PRIOR APPLICATION NUMBER: 60/267,459  
; PRIOR FILING DATE: 2001-02-08  
; Remaining Prior Application data removed - See file wrapper or PALM.

NUMBER OF SEQ ID NOS: 1391  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 697  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-072-012-697

Query Match 95.6%; Score 932; DB 15; Length 184;  
Best Local Similarity 93.5%; Pred. No. 1.4e-94;  
Matches 172; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGNGMKILPGLYIGNFKDARDAEQLSKNKKVTHLSVHDSARPMLGVKYLICIPAADSPS 60  
Db 1 MGSGMSQLPGLYIGNFKDARDAEQLSKNKKVTHLSVHDTARPMLGVKYLICIPAADTPS 60

Qy 61 QNLTRHPKESIKFTHCRLRGESCLVHCLAGVSRVTLVIAYIMTVDTFGWEDALHTVRA 120  
Db 61 QNLTRHPKESIKFTHCRLRGESCLVHCLAGVSRVTLVIAYIMTVDTFGWEDALHTVRA 120

Qy 121 GRSCANPNVGFQRLQEFKEHVEHGYRQWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180  
Db 121 GRSCANPNLGFQRLQEFKEHVEHGYRQWLKEEYGENPLRDAEAKNLAAPGILKYWAF 180

Qy 181 LRL 184  
Db 181 LRL 184

RESULT 11  
US-10-072-012-430  
; Sequence 430, Application US/10072012  
; Publication No. US20040033493A1  
; GENERAL INFORMATION:  
; APPLICANT: Tchernev, Velizar  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Zerhusen, Bryan  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Shinkets, Richard  
; APPLICANT: Li, Li  
; APPLICANT: Gangolli, Esha  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Anderson, David W.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Taupier Jr, Raymond J.  
; APPLICANT: Gusev, Vladimir Y.  
; APPLICANT: Colman, Steven D.  
; APPLICANT: Wolenc, Adam R.  
; APPLICANT: Pena, Carol E. A  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Grosse, William M.  
; APPLICANT: Alsobrook II, John P.  
; APPLICANT: Lepley, Denise M.  
; APPLICANT: Rieger, Daniel K.  
; APPLICANT: Burgess, Catherine E.  
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-258  
; CURRENT APPLICATION NUMBER: US/10/072,012  
; PRIOR FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: 60/265,102  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: 60/265,514  
; PRIOR FILING DATE: 2001-01-31  
; PRIOR APPLICATION NUMBER: 60/265,517  
; PRIOR FILING DATE: 2001-01-31  
; PRIOR APPLICATION NUMBER: 60/265,412  
; PRIOR FILING DATE: 2001-01-31  
; PRIOR APPLICATION NUMBER: 60/265,395  
; PRIOR FILING DATE: 2001-01-31  
; PRIOR APPLICATION NUMBER: 60/266,406  
; PRIOR FILING DATE: 2001-02-02

NPA

; PRIOR APPLICATION NUMBER: 60/266,767  
; PRIOR FILING DATE: 2001-02-05  
; PRIOR APPLICATION NUMBER: 60/267,057  
; PRIOR FILING DATE: 2001-02-07  
; PRIOR APPLICATION NUMBER: 60/266,975  
; PRIOR FILING DATE: 2001-02-07  
; PRIOR APPLICATION NUMBER: 60/267,459  
; PRIOR FILING DATE: 2001-02-08  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1391  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 430  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (40)..(46)  
; OTHER INFORMATION: Wherein Xaa is any amino acid.  
US-10-072-012-430

Query Match 94.7%; Score 923; DB 15; Length 184;  
Best Local Similarity 94.6%; Pred. No. 1.4e-93;  
Matches 174; Conservative 2; Mismatches 8; Indels 0; Gaps 0;  
  
Qy 1 MGNMKNILPGLYIGNFKDARDAGQLSKNKHVTHLSVHDSARPMLGKVKYLCIPAAADSPS 60  
Db 1 MGNMKNILPGLYIGNFKDARDAGQLSKNKHVTHLSVHDSARPMLGKVKYLCIPAAADSPS 60  
  
Qy 61 QNLTRHFKESIKFTHCRLRGESCLVHCLAGVSRSVTLVIAYIMTVTDFGWEDALHTVRA 120  
Db 61 QNLTRHFKESIKFTHCRLRGESCLVHCLAGVSRSVTLVIAYIMTVTDFGWEDALHTVRA 120  
  
Qy 121 GRSCANPNVGFQRLQEFKEHVEHQYRWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180  
Db 121 GRSCANPNVGFQRLQEFKEHVEHQYRWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180  
  
Qy 181 LRRL 184  
Db 181 LRRL 184

RESULT 12  
US-10-072-012-698  
; Sequence 698, Application US/10072012  
; Publication No. US20040033493A1  
; GENERAL INFORMATION:  
; APPLICANT: Tchernev, Velizar  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Zethusen, Bryan  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Shimkets, Richard  
; APPLICANT: Li, Li  
; APPLICANT: Gangolli, Esha  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Anderson, David W.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Taupier Jr, Raymond J.  
; APPLICANT: Gusev, Vladimir Y.  
; APPLICANT: Colman, Steven D.  
; APPLICANT: Wolenc, Adam R.  
; APPLICANT: Pena, Carol E. A  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Grosse, William M.  
; APPLICANT: Alsobrook II, John P.  
; APPLICANT: Lepley, Denise M.  
; APPLICANT: Kieger, Daniel K.  
; APPLICANT: Burgess, Catherine E.  
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-258  
; CURRENT APPLICATION NUMBER: US/10/072,012

NPA

; CURRENT FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: 60/265,102  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: 60/265,514  
; PRIOR FILING DATE: 2001-01-31  
; PRIOR APPLICATION NUMBER: 60/265,517  
; PRIOR FILING DATE: 2001-01-31  
; PRIOR APPLICATION NUMBER: 60/265,412  
; PRIOR FILING DATE: 2001-01-31  
; PRIOR APPLICATION NUMBER: 60/265,395  
; PRIOR FILING DATE: 2001-01-31  
; PRIOR APPLICATION NUMBER: 60/266,406  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 60/266,767  
; PRIOR FILING DATE: 2001-02-05  
; PRIOR APPLICATION NUMBER: 60/267,057  
; PRIOR FILING DATE: 2001-02-07  
; PRIOR APPLICATION NUMBER: 60/266,975  
; PRIOR FILING DATE: 2001-02-07  
; PRIOR APPLICATION NUMBER: 60/267,459  
; PRIOR FILING DATE: 2001-02-08  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1391  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 698  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: VARIANT  
; LOCATION: (40)..(46)  
; OTHER INFORMATION: Wherein Xaa is any amino acid.  
US-10-072-012-698

Query Match 94.7%; Score 923; DB 15; Length 184;  
Best Local Similarity 94.6%; Pred. No. 1.4e-93;  
Matches 174; Conservative 2; Mismatches 8; Indels 0; Gaps 0;  
  
Qy 1 MGNMKNILPGLYIGNFKDARDAGQLSKNKHVTHLSVHDSARPMLGKVKYLCIPAAADSPS 60  
Db 1 MGNMKNILPGLYIGNFKDARDAGQLSKNKHVTHLSVHDSARPMLGKVKYLCIPAAADSPS 60  
  
Qy 61 QNLTRHFKESIKFTHCRLRGESCLVHCLAGVSRSVTLVIAYIMTVTDFGWEDALHTVRA 120  
Db 61 QNLTRHFKESIKFTHCRLRGESCLVHCLAGVSRSVTLVIAYIMTVTDFGWEDALHTVRA 120  
  
Qy 121 GRSCANPNVGFQRLQEFKEHVEHQYRWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180  
Db 121 GRSCANPNVGFQRLQEFKEHVEHQYRWLKEEYGESPLQDAEAKNLAAPGILKFWAF 180  
  
Qy 181 LRRL 184  
Db 181 LRRL 184

RESULT 13  
US-10-803-738-2  
; Sequence 2, Application US/10803738  
; Publication No. US20050014222A1  
; GENERAL INFORMATION:  
; APPLICANT: Belmont, John  
; APPLICANT: Fletcher, Frederick  
; APPLICANT: Chen, Alice  
; APPLICANT: Jurecic, Roland  
; APPLICANT: Colicos, Suzanne  
; APPLICANT: Tan, Tse-Hua  
; APPLICANT: Zhou, Guisheng  
; TITLE OF INVENTION: Phosphatases Which Activate Map Kinase Pathways  
; FILE REFERENCE: 99-383-B  
; CURRENT APPLICATION NUMBER: US/10/803,738  
; CURRENT FILING DATE: 2004-03-18  
; PRIOR APPLICATION NUMBER: US/09/665,819A  
; PRIOR FILING DATE: 2000-09-20

; PRIOR APPLICATION NUMBER: US 60/155,068  
; PRIOR FILING DATE: 1999-09-21  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 205  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-803-738-2

Query Match 92.0%; Score 897; DB 17; Length 205;  
Best Local Similarity 90.5%; Pred. No. 1.2e-90;  
Matches 172; Conservative 3; Mismatches 5; Indels 10; Gaps 1;  
QY 1 MGNKMKILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLEGVKYLICIPAADS 60  
DB 1 MGNKMKILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLEGVKYLICIPAADS 60  
QY 61 QNLTRHFKESIKFIECHLRGESCILVHCLAGVSRVTLVIAYIMTVDTFGWEDALHTVRA 120  
DB 61 QNLTRHFKESIKFIECHLRGESCILVHCLAGVSRVTLVIAYIMTVDTFGWEDALHTVRA 120  
QY 121 GRSCANPNVGFQRLQOEFEKHEVHQYRWLKEEYGESPLQDAEAKNITL 170  
DB 121 GRSCANPNVGFQRLQOEFEKHEVHQYRWLKEEYGESPLQDAEAKNITL 170  
QY 171 APGLKFWAF 180  
DB 181 QGARRWSSF 190

RESULT 14  
US-10-803-738-4  
; Sequence 4, Application US/10803738  
; Publication No. US20050014222A1  
; GENERAL INFORMATION:  
; APPLICANT: Belmont, John  
; APPLICANT: Fletcher, Frederick  
; APPLICANT: Chen, Alice  
; APPLICANT: Jurecic, Roland  
; APPLICANT: Colicos, Suzanne  
; APPLICANT: Tan, Tse-Hua  
; APPLICANT: Zhou, Guisheng  
; TITLE OF INVENTION: Phosphatases Which Activate Map Kinase Pathways  
; FILE REFERENCE: 99-383-B  
; CURRENT APPLICATION NUMBER: US/10/803,738  
; PRIOR FILING DATE: 2004-03-18  
; PRIOR APPLICATION NUMBER: US/09/665,819A  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR FILING DATE: 1999-09-21  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 205  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-803-738-4

Query Match 86.5%; Score 843; DB 17; Length 205;  
Best Local Similarity 92.3%; Pred. No. 1.2e-84;  
Matches 156; Conservative 11; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MGNKMKILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLEGVKYLICIPAADS 60  
DB 1 MGSMSQLPGLYIGNFKDARDAEQLSKNKVTHILSVHDTARPMLEGVKYLICIPAADS 60  
QY 61 QNLTRHFKESIKFIECHLRGESCILVHCLAGVSRVTLVIAYIMTVDTFGWEDALHTVRA 120  
DB 61 QNLTRHFKESIKFIECHLRGESCILVHCLAGVSRVTLVIAYIMTVDTFGWEDALHTVRA 120  
QY 121 GRSCANPNVGFQRLQOEFEKHEVHQYRWLKEEYGESPLQDAEAKNITL 169

DB 121 GRSCANPNLGFQRLQOEFEKHEVHQYRWLKEEYGENFLRDAEAKNITL 169

RESULT 15  
US-10-803-738-5  
; Sequence 5, Application US/10803738  
; Publication No. US20050014222A1  
; GENERAL INFORMATION:  
; APPLICANT: Belmont, John  
; APPLICANT: Fletcher, Frederick  
; APPLICANT: Chen, Alice  
; APPLICANT: Jurecic, Roland  
; APPLICANT: Colicos, Suzanne  
; APPLICANT: Tan, Tse-Hua  
; APPLICANT: Zhou, Guisheng  
; TITLE OF INVENTION: Phosphatases Which Activate Map Kinase Pathways  
; FILE REFERENCE: 99-383-B  
; CURRENT APPLICATION NUMBER: US/10/803,738  
; CURRENT FILING DATE: 2004-03-18  
; PRIOR APPLICATION NUMBER: US/09/665,819A  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: US 60/155,068  
; PRIOR FILING DATE: 1999-09-21  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 138  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: mJKAP  
US-10-803-738-5

Query Match 70.8%; Score 690; DB 17; Length 138;  
Best Local Similarity 93.5%; Pred. No. 5.9e-68;  
Matches 129; Conservative 7; Mismatches 2; Indels 0; Gaps 0;  
QY 5 MNKILPGLYIGNFKDARDAEQLSKNKVTHILSVHDSARPMLEGVKYLICIPAADS 64  
DB 1 MSQILPGLYIGNFKDARDAEQLSKNKVTHILSVHDTARPMLEGVKYLICIPAADS 60  
QY 65 RHFKESIKFIECHLRGESCILVHCLAGVSRVTLVIAYIMTVDTFGWEDALHTVRA 124  
DB 61 RHFKESIKFIECHLRGESCILVHCLAGVSRVTLVIAYITTTDFGWDALHTVRA 120  
QY 125 ANPNVGFQRLQOEFEKHE 142  
DB 121 ANPNLGFQRLQOEFEKHE 138

Search completed: July 21, 2005, 19:26:24  
Job time : 72 secs

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